#### STIC-Biotech/ChemLib

103886

F	rom:
_	

Chan, Christina

Sent: To:

Monday, September 15, 2003 9:05 AM Rao, Manjunath N.; STIC-Biotech/ChemLib

Subject:

RE: RUSH sequence search request for 10/083,336

Please rush. Thanks Chris

Chris Chan

TC 1600 New Hire Training Coordinator and SPE 1644 308-3973 CM-1, 9B19

----Original Message-----

From:

Rao, Manjunath N.

Sent:

Monday, September 15, 2003 9:00 AM

To:

Chan, Christina

Subject:

RUSH sequence search request for 10/083,336

Hello Christina,

Please authorize the request below as RUSH. The reason being this is an amended due this biweek and the previous search I did is incomplete.

Thanks Manjunath

From: Manjunath N. Rao

Art Unit 1652, Room 10A11 Mail Box in Room 10D 01

Phone: 306-5681

Date:

9-15-03

Edward Hart

Technica: Info. Specialist

STIC/Biotech

CMI 6B02 Tel: 305-9203

Please search the following as soon as possible for application with serial number 10/083,336

1. SEQ ID NO:1, 2, 3, and 4 against all <u>commercial protein databases</u> including <u>issued</u> <u>patents database</u> and <u>pending application database</u> and provide a print of <u>all</u> results.

If you have any questions please call me at the above phone number.

Searcher: \_\_\_\_\_\_Phone: \_\_\_\_\_\_
Location: \_\_\_\_\_\_
Date Picked Up: \_\_\_\_\_\_
Date Completed: \_\_\_\_\_
Searcher Prep/Review: \_\_\_\_\_
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Online time: \_\_\_\_\_

TYPE OF SEARCH:

NA Sequences:

AA Sequences:

Structures:

Bibliographic:

Litigation:

Full text:

Patent Family:

Other:

VENDOR/COST (where applic.)
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Lexis/Nexis:\_
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WWW/Internet:

Other (specify):

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Thanks

103886

Manjunath N. Rao, Ph.D. Biotechnology Patent Examiner Art Unit 1652, Room 10A11 Mail Box in 10D01 Crystal Mall 1, USPTO.

Searcher:
Phone:
Location:
Date Picked Up:
Date Completed:
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TYPE OF SEARCH:
NA Sequences:
AA Sequences:
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# STIC Search Report Biotech-Chem Library

### STIC Database Tracking Number: 103886

TO: Manjunath N Rao

Location: cm1/10a11/10d01

Art Unit: 1652

Tuesday, September 16, 2003

Case Serial Number: 10/083336

From: Edward Hart

**Location: Biotech-Chem Library** 

CM1-6B02

Phone: 305-9203

edward.hart@uspto.gov

#### Search Notes

Examiner Rao,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

**Edward Hart** 





### STIC SEARCH RESULTS

### **Biotech-Chem Library**

Questions about the scope or the results of the search? Contact the searcher or contact:

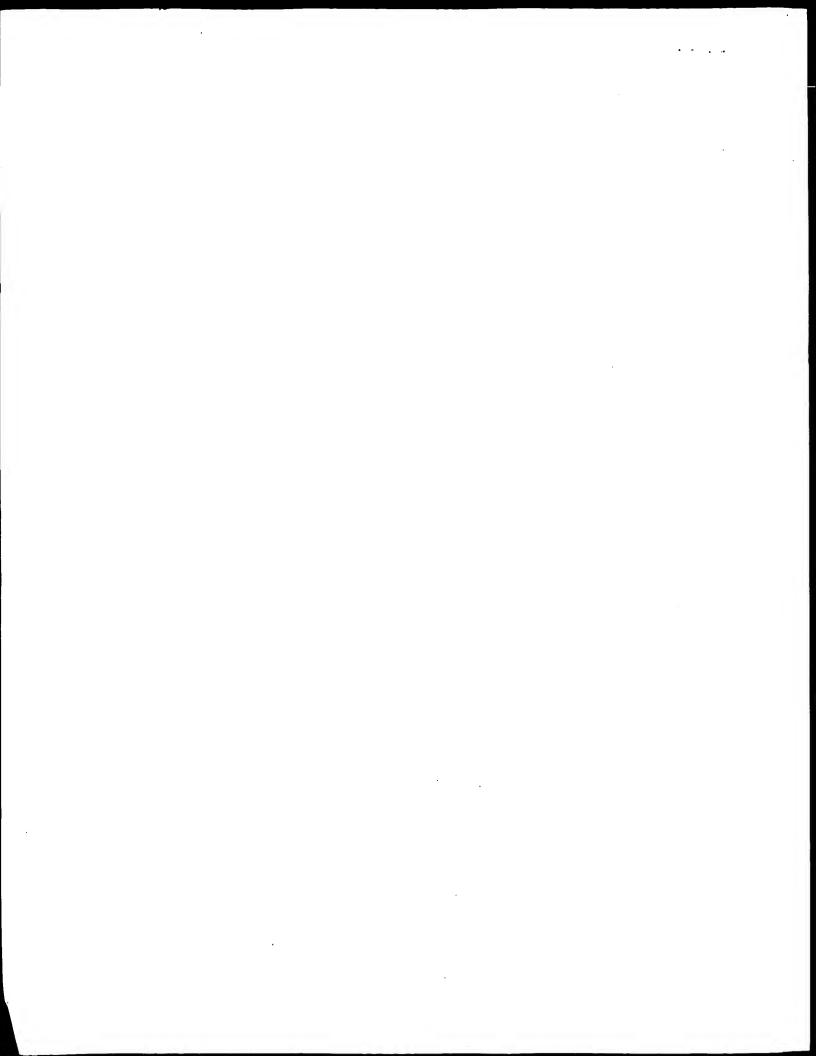
Mary Hale, Information Branch Supervisor 308-4258, CM1-1E01

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>	I am an examiner in Workgroup: Example: 1610
>	Relevant prior art found, search results used as follows:
	☐ 102 rejection
	☐ 103 rejection
	Cited as being of interest.
	Helped examiner better understand the invention.
	Helped examiner better understand the state of the art in their technology.
	Types of relevant prior art found:
	☐ Foreign Patent(s)
	<ul> <li>Non-Patent Literature         (journal articles, conference proceedings, new product announcements etc.)</li> </ul>
>	Relevant prior art not found:
	Results verified the lack of relevant prior art (helped determine patentability)
	Results were not useful in determining patentability or understanding the invention.
Cor	nments:

Drop.off.or send completed forms to STIC/Biotech-Chem Library CM1 — Girc. Desk





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Title:
Perfect score:
Sequence:
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Maximum Match 100%
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# ALIGNMENTS

RESULT 1 AAW25787

AAW25787 standard; Protein; 576 AA.

Castorbean ricin.

25-MAR-2003 27-MAR-1998

(updated)
(first entry)

AAW25787;

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04-AUG-1993;
                                                                                                                                     Ricin; cytotoxin; hybrid protein; cell delivery; cell binding ligand; translocation domain; diphtheria toxin B'; interleukin-2; T-cell lymphoma; organ rejection; therapy.
               16-SEP-1997.
                              US5668255-A
                                                     Domain
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07-JUN-1984;
25-APR-1985;
07-JUN-1985;
22-DEC-1989;
14-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptors, resulting in cessation of protein synthesis and death of target cells. Claimed hybrid proteins comprise a translocation domain and a cell binding domain from e.g. a hormone, growth factor or polypeptide toxin. The hybrid molecules can be used for the delivery of agents (e.g. therapeutic genes, toxins, detectable labels) into cells. The use of a translocation mechanism ensures that the hybrid will be effective in relatively low doses, since a high proportion of the substance of interest will be taken into the targeted cells. The hybrid molecules can be manufactured as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This polypeptide comprises the castorbean cytotoxin, ricin. DNA (see AAT91638) encoding the enzymatic A domain and a portion of the A-to-B linker peptide of ricin was used to construct a ricin-diphtheria toxin B'-interleukin-2 gene that was expressed in E. coli. The hybrid protein can be isolated and used to treat conditions involving over-production of cells bearing IL2 receptors, such as certain T-cell lymphomas and organ transplant rejection crises. The hybrid inactivates ribosomes in cells bearing IL2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           single hybrid recombinant protein, permitting reproducibility, consistency, and the precise control of composition. (Updated on 25-MAR-2003 to correct PF field.)
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RESULT 2
AAY55892
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protein comprising three parts: (a) the first part comprises a portion of the binding domain of a cell-binding polypeptide ligand allowing the hybrid protein to bind to an animal cell; (b) the second part comprises a portion of a translocation domain of a naturally occurring protein selected from diphtheria toxin, botulinum neurotoxin, ricin, cholera toxin, T toxin, C3 toxin, shiga-like toxin, pertussis toxin and tetanus toxin, which translocate the third part of the across the cytoplasmic membrane into the cytosol of the cell; and (c) the third part comprises a polypeptide entity to be introduced into the cell, which is non-native to the naturally occurring protein of (b). This sequence represents the Castor bean ricin toxin sequence for use in generating the bybrid of the hybrid of the comprises the castor bean ricin toxin sequence for use in generating the bybrid of the hybrid of the comprises the castor bean ricin toxin sequence for use in generating the hybrid of the hybrid of the castor bean ricin toxin sequence for use in generating the hybrid of the castor bean ricin toxin sequence for use in generating the hybrid of the hybrid of the castor bean ricin toxin sequence for use in generating the hybrid of the castor bean ricin toxin sequence for use in generating the hybrid of the castor bean ricin toxin sequence for use in generating the hybrid of the castor bean ricin toxin sequence for use in generating the hybrid of the castor bean ricin toxin sequence for use in generating the hybrid of the castor bean ricin toxin sequence for use in generating the hybrid of the castor bean ricin toxin sequence for use in generating the hybrid of the castor bean ricin toxin sequence for use in generating the hybrid of the castor bean ricin toxin sequence for use in generating the hybrid of the castor bean ricin toxin sequence for use in generating the hybrid of the castor bean ricin toxin sequence for use in generating the hybrid of the castor bean ricin toxin sequence for use in generating the hybrid of the castor be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-APR-1985;
07-JUN-1985;
22-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant; hybrid; binding domain; ligand; animal cell; diphtheria; translocation domain; botulinum; neurotoxin; ricin; cholera; tetanus; shiga-like toxin; pertussis; translocation; cytoplasmic membrane; HIV cytosol; therapy; genetic deficiency disease; enzyme; co-factor; poise adipocyte; cancer; virus; infection; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY55892 standard; Protein; 576 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAZ30663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murphy JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1984;
27-JUN-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ricinus communis.
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                                                                                                                                                                                                                                                                                                                                           Example 4; Fig 11; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                       Recombinant DNA molecule encoding a three part hybrid the treatment of Alds and genetic deficiency diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-632431/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SERA-) SERAGEN
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89US-0456095.
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91US-0722484.
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RESULT 3
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AC AAY7
XX
DT 05-P
DT 05-P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               particular enzyme or a scarce precursor or cofactor, to directing toxins or other poisons to destroy particular cells (such as adipocytes, cancer cell, or virus infected cells), to counteracting viral infections such as HIV, by introducing appropriate antibodies to viral process. It is also involved in the process of getting non-therapeutic substances such as detectable labels into cells.
                           Ricin; toxin; hybrid protein; translocation domain; cell destruction; cell binding domain; genetic deficiency disease; cell targetting; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention. The hybrid molecule enables the direction of appropriate therapy to affected cells, allowing them to function properly and alleviate or cure the disease. The hybrid is especially used in treating genetic deficiency diseases, by delivering to affected cells an enzyme
                                                                                                                                                                         AAY78592 standard; Protein; 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                           communis ricin protein sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QFSLLIRPVVPNFNADVCMDPEPIVRIVGRNGLCVDVRDGRFHNGNAIQLWPCKSNTDAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TLENSWGRLSTAIQESNQGAFASPIQLQRRNGSKFSVYDVSILIPIIALMVYRCAPPPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRTRIRYNRRSAPDPSVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EAISALYYYSTGGTQLFTLARSFIICIQMISEAARFQYIEGEMRTRIRYNRRSAPDPSVI
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                                                                                                                                                                                                                                                                                                                                               EKAEQQWALYADGSIRPQQNRDNCLTSDSNIRETVVKILSCGPASSGQRWMFKNDGTILN
                enzyme delivery;
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                                                                                                           (first entry)
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                anti-viral;
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                VIH.
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                                                                                                                                                                                                                                                                                                                   540
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QΥ

Q

60

Matches 576; Best Local Similarity

Conservative

0;

Mismatches

0;

Indels

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Q Вþ

121 61 61

AGNSAYFFHDDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPLE

180

120

**AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPLE** 

RAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYR

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This sequence represents the Ricinus communis ricin protein sequence. The CC toxin can be included in the hybrid protein of the invention and used to CC destroy or modify the cell that the hybrid protein is targeted to. The CC hybrid protein comprises a first part which is a portion of the binding CC domain of a cell of an animal. The second part comprises a portion of a CC translocation domain of a naturally occurring protein (e.g. the third part across the cytoplasmic membrane and into the cytosol of CC the third part across the cytoplasmic membrane and into the cytosol of CC into the cell, where each of the first and third part is non-native with CC respect to naturally occurring protein, and the covalent bond attaching CC the second and third part is cleavable. The toxin represented by the CC present sequence can form part of the third portion of the hybrid CC protein. The cell binding domain binds to a specific cell and the CC translocation domain transfers the hybrid molecule across the cell CC translocation domain through a cleavable bond, can then carry out its CC function. The hybrid molecules are useful for treating genetic deficiency CC diseases by delivering to affected cells an enzyme supplying the missing CC scarce precursor or cofactor, to direct toxins or other poisons to CC destroy particular cells (such as adipocytes, cancer cells, or virus-infected cells), and to counteract viral infections such as HIV by introducing into appropriate cells antibodies to viral proteins.
                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-JUN-1985;
22-DEC-1989;
14-JUN-1990;
04-AUG-1993;
                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New two-part hybrid protein comprising a translocation domain and a cell-binding domain, for treating genetic deficiency diseases, cancer and HIV infections -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-JUN-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; Fig 11; 32pp; English.
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25-APR-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SERA-) SERAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIV infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2000-160390/14
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                                                      576 AA;
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89US-0456095.
90US-0538276.
93US-0102387.
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85US-0726808
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100.0%;
Score 3051; DB 21; Pred. No. 1.8e-252;
               Length
                  576;
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RESULT 4
AAG78301
ID AAG7
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                   N-PSDB; AAI64138
                                                                           Keener WK,
                                                                                                                                                    15-FEB-2000; 2000US-0182759
                                                                                                                                                                                     15-FEB-2001; 2001WO-US05282
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                                                                                                              (BECH-) BECHTEL BWXT IDAHO LLC
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                                      2001-581908/65
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/note= "Cleaved during
315..576
                                                                                                                                                                                                                                                                                                                                                                                          /label= Ricin_A_chain
/note= "N-glycosidase"
303..314
                                                                                                                                                                                                                                                                                               /note= "Galactose/N-acetylgalactosamine-binding lectin'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Signal peptide
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 AAG78302 standard; Protein; 576
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Novel composition comprising toxin e.g., ricin based antiviral compound useful for treating viral infections such as human immunodeficiency
virus infection.
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Page 50-54; 66pp; English.

invention is useful for treating human immunodeficiency virus infection and other viral infections, especially retroviral infections. The antiviral agent is activated in viral particles or early-stage infected cells, killing the cells upon infection and effectively preventing the integration of the viral genome into the host genome thereby preventing the latency/rebound problem. The agent enters all HIV susceptible cells, and not just cells known to act as host cells for the virus. The antiviral agent remains inert in a cell until degraded in it, unless the cell is infected with the virus, where the viral protease activates it. The sequence relates to preproricin protein encoded by the DNA sequence given in AAI64138. The invention relates to a novel toxin (e.g., ricin) based antiviral agent which is toxic to virus-infected cells, but non-toxic to uninfected cells. The invention has anti-HIV and virucide activities. Its mechanism of action is through inactivation of cellular ribosomes and enhancement of binding of the antiviral agent to galactose residues on cell surfaces, and its cellular internalisation. The

Sequence 576 AA;

DB 22;

Length 576;

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Matches
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                541 LYSGLVLDVRASDPSLKQIILYPLHGDPNQIWLPLF 576
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                                                                                                                            LAATSGNSGTTLTVQTNIYAVSQGWLPTNNTQPFVTTIVGLYGLCLQANSGQVWIEDCSS
                                                                                                                                        LAATSGNSGTTLTVQTNIYAVSQGWLPTNNTQPFVTTTVGLYGLCLQANSGQVWIEDCSS
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LYSGLVLDVRASDPSLKQIILYPLHGDPNQIWLPLF
                                                               EKAEQQWALYADGS1RPQQNRDNCLTSDSN1RETVVK1LSCGPASSGQRWMFKNDGT1LN
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Pred. No. 1.8e-252;
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                                                                                                          Query Match
Best Local
                                                                                         Matches
                                                                                                                                                                       Sequence
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DB; AAI64139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              composition comprising toxin e.g., ricin based antiviral compound l for treating viral infections such as human immunodeficiency infection.
                                                                                         576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      r bean plant; preproricin; ricin; A chain; B chain; immunodeficiency virus infection; HIV; toxin; antiviral agent; viral infection; anti-HIV; virucide activity; viral protease.
                                                                                                          Similarity
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                     MKPGGNTIVIWMYAVATWLCEGSTSGWSFTLEDNNIFPKQYPIINFTTAGATVQSYTNFI
    MKPGGNTIVIWMYAVATWLCFGSTSGWSFTLEDNNIFPKQYPIINFTTAGATVQSYTNFI
                                                                                                                                                                       576 AA;
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                                                                                                        100.
                                                                                                          .08;
                                                                                    0;
                                                                                Score 3051; DB 22;
Pred. No. 1.8e-252;
; Mismatches 0;
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                                                                                  Indels
                                                                                                                       Length
                                                                                  0;
                                                                                  Gaps
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AAP70325
ID AAP7
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AC AAP7
XX
  DT COS SOCIAL CONTRACTOR CONTRACT
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                                                          07-MAR-1986;
                                                                                                                                               23-SEP-1987
                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003
18-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAP70325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP70325 standard; protein; 574 AA
(CETU ) CETUS CORP.
                                                                                                      13-NOV-1986;
                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                 Ricinus
                                                                                                                                                                                                                                                                                                                                                                                                                                      plant toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  541
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                                                                                                                                                                                                                                                                                                                                                                                                 communis
                                                                                                                                                                                                                                                                                                                                                                                                                                                          toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LAATSGNSGTTLTVQTNIYAVSQGWLPTNNTQPFVTTIVGLYGLCLQANSGQVWIEDCSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LYSGLVLDVRASDPSLKQIILYPLHGDPNQIWLPLF 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TLENSWGRLSTAIQESNQGAFASPIQLQRRNGSKFSVYDVSILIPIIALMVYRCAPPPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EKAEQQWALYADGSIRPQQNRDNCLTSDSNIRETVVKILSCGPASSGQRWMFKNDGTILN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QLWTLKRDNTIRSNGKCLTTYGYSPGVYVMIYDCNTAATDATRWQIWDNGTIINPRSSLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QFSLLIRPVVPNFNADVCMDPEPIVRIVGRNGLCVDVRDGRFHNGNAIQLWPCKSNTDAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OFSLLIRPVVPNENADVCMDPEPIVRIVGRNGLCVDVRDGRFHNGNAIQLWPCKSNTDAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TLENSWGRLSTAIQESNQGAFASPIQLQRRNGSKFSVYDVSILIPIIALMVYRCAPPPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRTRIRYNRRSAPDPSVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPLE 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LAATSGNSGTTLTVQTNIYAVSQGWLPTNNTQPFVTTIVGLYGLCLQANSGQVWIEDCSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ricinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein; cytotoxic; cytostatic;
                                                            86US-0837583
                                                                                                      86EP-0308877.
                                                                                                                                                                                                                                                 /note="A-chain"
313..574
                                                                                                                                                                                                                                                                                           34..300
                                                                                                                                                                                                                              /note="B-chain"
                                                                                                                                                                                                                                                                                                            /note="Leader"
                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 communis castor beans ricin toxin (RT or ricin) by pRT17.
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castor bean

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The full-length sequences encoding ricin A (AAN70520), ricin D (AAN70525), putative ricin E (AAN70520) and RCA (AAN70524) in precursor form were obtd. using messenger RNA to obtain a cDNA library, and then probing the library to retrieve the desired cDNA inserts. The library was probed using the 35-mer given in AAN70514. Figure 4 (see AAN70520, AAN70521) AAN70521) shows the nucleotide sequences of three cc plasmids contg. cDNA inserts obtd. by probing a cDNA library for sequences encoding ricin B using the probe in AAN70517. The cDNA linserts can be placed into expression vectors. Site-directed mutagenesis may be used to place an AFG start codon and a Hindill cc site at the beginning of the mature protein (see AAN70518). The ccoding sequences of the inserts can be ligated into expression vectors contg. the phoA promoter-operator and leader sequence (AAN70533) and suitable retroregulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New non-glycosylated ricin precursor and toxin etc. - are prepd
by recombinant DNA procedures with specific isolation steps for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Piatak M;
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DB; AAN70525.
 541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPLEEA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYRAG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYRAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGGNTIVIWMYAVATWLCFGSTSGWSFTLEDNNIFPKQYPIINFTTAGATVQSYTNFIRA 62
AEQQWALYADGSIRPQQNRDNCLTSDSNIRETVVKILSCGPASSGQRWMFKNDGTILNLY 542
                                                                                                                                                             ATSGNSGTTLTVQTNIYAVSQGWLPTNNTQPFVTTIVGLYGLCLQANSGQVWIEDCSSEK 482
                                                                                                                                                                                                                                                      WTLKRDNTIRSNGKCLTTYGYSPGVYVMIYDCNTAATDATRWQIWDNGTIINPRSSLVLA 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRTRIRYNRRSAPDPSVITL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PGGNTIVIWMYAVATWLCFGSTSGWSFTLEDNNIFPKQYPIINFTTAGATVQSYTNFIRA 60
                                    SGLVLDVRASDPSLKQIILYPLHGDPNQIWLPLF 576
                                                                      AEQQWALYADGSIRPQQNRDNCLTSDSNIRETVVKILSCGPASSGQRWMFKNDGTILNLY
                                                                                                                                              ATSGNSGTTLTVQTNIYAVSQGWLPTNNTQPFVTTIVGLYGLCLQANSGQVWIEDCSSEK
                                                                                                                                                                                                                    WTLKRDNTIRSNGKCLTTYGYSPGVYVMIYDCNTAATDATRWQIWDNGTIINPRSSLVLA
                                                                                                                                                                                                                                                                                          SLLIRPVVPNFNADVCMDPEPIVRIVGRNGLCVDVRDGRFHNGNAIQLWPCKSNTDANQL
                                                                                                                                                                                                                                                                                                             SLLIRPVVPNFNADVCMDPEPIVRIVGRNGLCVDVRDGRFHNGNAIQLWPCKSNTDANQL
                                                                                                                                                                                                                                                                                                                                                              ENSWGRLSTAIQESNQGAFASPIQLQRRNGSKFSVYDVSILIPIIALMVYRCAPPPSSQF
                                                                                                                                                                                                                                                                                                                                                                                                 ENSWGRLSTAIQESNQGAFASPIQLQRRNGSKFSVYDVSILIPIIALMVYRCAPPPSSQF 302
                                                                                                                                                                                                                                                                                                                                                                                                                                       ISALYYYSTGGTQLPTLAGSFIICIQMISEAARFQYIEGEMRTRIRYNRRSAPDPSVITL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPLEEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  soluble prods.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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Pred. No. 5.2e-251;
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 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 574;
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RESULT 7
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Best Local
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                                                                                                                                                                                                                                   Recombinant baculovirus vector is capable of introducing ricin gene virus genome, allowing creation of a insect cell/baculovirus ricin expression system.
                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                              expression system.
                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                        24-JUL-1987;
08-FEB-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                     20-JUL-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Baculovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ricin; toxin; baculovirus; muteins; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA sequence of ricin toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JUL-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAP94793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP94793 standard;
                                                                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                                                       Recombinant baculovirus transfer vectors -
used for prodn. of ricin toxin in a baculovirus insect cell
                                                                                                                                                                                                                                                                                                                                                                 Houston LL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO8901037-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                               WPI; 1989-061173/08
                                                                                                                                                                                                                                                                                                                                                                                     (CETU ) CETUS CORP.
                                                                                                                                                                                    Local
                   181
                                      183
                                                         121
243 ENSWGRLSTAIQESNQGAFASPIQLQRRNGSKFSVYDVSILIPIIALMVYRCAPPPSSQF
                                                                                                                                                                            573;
                                                                                                61
                                                                                                                                                        w
                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                      AAN91039
                                                                                                         VRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYRAG
                                                                                                                                     ISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRTRIRYNRRSAPDPSVITL
                                                                     NSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPLEEA
                                                                                                VRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYRAG
                                                          NSAYFFHGDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPLEEA
                   ISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRTRIRYNRRSAPDPSVITL
                                                                                                                                                                                                                  574 AA;
                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                           Page -;
                                                                                                                                                                                                                                                                                                                                                                 Lane JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                       87US-0077126
88US-0153778
                                                                                                                                                                                                                                                                                                                                                                                                                                     88WO-US02442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label=A-chain
301..574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label=Leader peptide
36..300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label=B-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein;
                                                                                                                                                                                                                                                                           85pp;
                                                                                                                                                                                     99.4%;
                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            574
                                                                                                                                                                            Score 3032; DI
Pred. No. 7.7e
0; Mismatches
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                                                                                                                                                                                    ; DB 10;
7.7e-251;
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                                                                                                                                                                                                 Length
                                                                                                                                                                                                 574;
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302

122

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RESULT 8
AAP70326
ID AAP70326
ID AAP70326
ID AAP70326
AAP70326
AAP70XX 20
DT 25-W
DT 21-W
XX Sequ
XX Lect
XX Lect
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XX Plar
XX Plar
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       The full length sequences (AAN70525) putative ricin
                                                                                                                  New non-glycosylated ricin precursor and toxin etc. - are post recombinant DNA procedures with specific isolation steps purer and soluble prods.
                                                                                                                                                                                                                                                                                         Piatak M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence of Ricinus communis (castor bean) Ricin toxin (RT or ricin) E precursor encoded by pRT38.
                                                                      Disclosure; Fig 14(1-2); 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                            07-MAR-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-NOV-1986;
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21-MAY-1991
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DB; AAN70526.
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/note= "A-chain"
315..576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "B-chain"
  encoding ricin A E (AAN70526) and
(AAN70520), ricin
RCA (AAN70524) in
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steps for
precursor
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       form were obtained, using the messenger RNA to obtain a cDNA library, and then probing the library to retrieve the desired cDNA inserts. The library was probed using the 35-mer given in AAN70514. Figure 4 (see AAN70520, AAN70521, AAN70522), shows the nucleotide sequences of three plasmids containing cDNA inserts obtained by probing a cDNA library for sequences encoding ricin B using the probe in AAN70517. The cDNA inserts can be placed into expression vectors. Site-directed mutagenesis may be used to place an ANG start codon and a HindIII site at the beginning of the mature protein, (see AAN70518). The coding sequences of the inserts can be ligated into expression vectors containing the PhoA promoter-operator and leader sequence (AAN70523) and suitable retroregulators.
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                           541 LYSGLVLDVRASDPSLKQIILYPLHGDPNQIWLPLF 576
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                                                                                                                      QFSLLIRPVVPNENADVCMDPEPIVRIVGRNGLCVDVRDGRFHNGNAIQLMPCKSNTDAN 360
                                                                                                                                                                                                     LYNGLVLDVRRSDPSLKQIIVHPFHGNLNQIWLPLF
                                                              EKAEQQWALYADGSIRPQQNRDNCLTTDANIKGTVVKILSCGPASSGQRWMFKNDGTILN
                                                                             EKAEQQWALYADGSIRPQQNRDNCLTSDSNIRETVYKILSCGPASSGQRWMFKNDGTILN
                                                                                                                                                                                        QLWTLKRDNTIRSNGKCLTTYGYSPGVYVMIYDCNTAATDATRWQIWDNGTIINPRSSLV
                                                                                                                                                                                                                                                                                                                TLENSWGRLSTAIQESNQGAFASPIQLQRRNGSKFSVYDVSILIPIIALMVYRCAPPPSS
                                                                                                                                                                                                                                                                                                                                  TLENSWGRLSTAIQESNQGAFASPIQLQRRNGSKFSYYDVSILIPIIALMYYRCAPPPSS
                                                                                                                                                                                                                                                                                                                                                                                             EAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRTRIRYNRRSAPDPSVI
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97.4%;
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Pred. No. 3.7e-247;
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RESULT 9
AAP50166
AAP50166 standard; Protein; 565
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Sequence of preproricin encoded by pRCL617

16-OCT-1991

(first entry)

Toxin; anti-tumour therapy

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Best Local S
Matches 563
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15-JUL-1983;
15-JUL-1983;
                                                                                                                                                                                                                                             preproricin is the whole polypeptide encoded by AAN50202 and the DNA encoding this is claimed. Proricin is obtained from preproricin by removal of the AA leader sequence. The linker AA sequence which is present in the precursor polypeptide is enzymatically removed in the cell to separate the A and B chains, which are joined by a disulphide bridge during the formation of the ricin molecule itself. This linker region as well as the presumptive amino terminal leader
                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                      or signal
                                                                                                                                                                                                                                                                                                                        Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                 Lcrd JM,
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                                                                                                                                                                                                                                                                                                                                         New DNA sequences coding for ricin type plant toxin - mutants, and modified vectors and host microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                 (UYWA-) UNIV WARWICK.
                                                                                                                                                                                Local Similarity
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                                      192
                                                         121
                    181
                                                                                                                                                                      563;
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                                                                                                       72 DVRHEIPVLPNRVGLPINORFILVELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFFPD
                                                                                                                                 AAN50202
                                                                                             DVRHDIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPD
                                                                 NQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPLEEAISALYYYST
 AIQESNQGAFASPIQLQRRNGSKFSVYDVSILIPIIALMVYRCAPPPSSQFSLLIRPVVP
                     GGTQLPTLARSF1ICIQMISEAARFQYIEGEMRTRIRYNRRSAPDPSVITLENSWGRLST
                                     GGTQLPTLARSFIICIQMISEAARFQYIEGEMRTRIRYNRRSAPDPSVITLENSWGRLST
                                                         NQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPLEEAISALYYYST
                                                                                                                                                                                                                             by Funatsu et
                                                                                                                                                                                                                                     sequence are not present in the sequences already
                                                                                                                                                                                                                                                                                                                                                                                                 Roberts LM,
                                                                                                                                                                                                           565 AA;
                                                                                                                                                                                                                                                                                                                       Page 30-30c; 40pp; English.
                                                                                                                                                                       Conservative
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83GB-0019265.
83CH-0019265.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= N-linked glycosylation 438..440
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/label= N-linked glycosylation
398..400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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                                                                                                                                                                      Score 2980; DB 6;
Pred. No. 2.1e-246;
1; Mismatches 1;
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                     Novel composition comprising toxin e.g., \boldsymbol{r} useful for treating viral infections such virus infection.
                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                                                                                                                    15-NOV-2001
   Disclosure; Page 47-50; 66pp; English
                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                               Peptide
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Castor bean plant; preproricin; ricin; A chain; B chain; human immunodeficiency virus infection; HIV; toxin; antiviral agent; retroviral infection; anti-HIV; virucide activity; viral protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ricinus communis.
                                                                                                                                                                                                                                                                                                               WO200160393-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Castor bean preproricin protein
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                                                     WPI; 2001-581908/65
N-PSDB; AAI64137.
                                                                                                                                                                                          16-FEB-2000; 2000US-0182759
                                                                                                                                                                                                                                 15-FEB-2001; 2001WO-US05282
                                                                                                                                                     (BECH-) BECHTEL BWXT IDAHO LLC.
                                                                                                                                                                                                                                                                        23-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DGSIRPQQNRDNCLTSDSNIRETVVKILSCGPASSGQRWMFKNDGTILNLYSGLVLDVRR 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "N-glycosidase" 291..302
                                                                                                                                                                                                                                                                                                                                                                                         /label= Linker_peptide
/note= "Cleaved during activation of ricin"
303..565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= Signal peptide 25..290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                      /note= "Galactose/N-acetylgalactosamine-binding
                                                                                                                                                                                                                                                                                                                                                                          Ricin_B_chain
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ricin based antiviral compound h as human immunodeficiency
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RESULT 11
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Best Local
25-MAR-2003
02-JUL-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention is useful for treating human immunodeficiency virus infection and other viral infections, especially retroviral infections. The antiviral agent is activated in viral particles or early stage infected cells, killing the cells upon infection and effectively preventing the integration of the viral genome into the host genome thereby preventing the latency/rebound problem. The agent enters all HIV susceptible cells, and not just cells known to act as host cells for the virus. The antiviral agent remains inert in a cell until degraded in it, unless the cell is infected with the virus, where the viral protease activates it.
                                                                                                         AAP60240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence relates to preproricin protein encoded by the DNA sequence given in AAI64137. The invention relates to a novel toxin (e.g., ricin) based antiviral agent which is toxic to virus-infected cells, but non-toxic to uninfected cells. The invention has anti-HIV and virucide activities. Its mechanism of action is through inactivation of cellular ribosomes and enhancement of binding of the antiviral agent to galactose residues on cell surfaces, and its cellular internalisation. The
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                                                                                                         standard;
                                                                                                                                                                                                                SDPSLKQIILYPLHGDPNQIWLPLF
                                                                                                                                                                                                                                       SDPSLKQIILYPLHGDPNQIWLPLF 576
                                                                                                                                                                                                                                                                                                   DGSIRPQQNRDNCLTSDSNIRETVVKILSCGPASSGQRWMFKNDGTILNLYSGLVLDVRR
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                                                                                                                                                                                                                                                                                                                                                                                                             LTVQTNIYAVSQGWLPTNNTQPFVTTIVGLYGLCLQANSGQVWIEDCSSEKAEQQWALYA 491
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AIQESNQGAFASPIQLQRRNGSKFSVYDVSILIPIIALMVYRCAPPPSSQFSLLIRPVVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPLEEAISALYYYST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGTQLPTLARSFIICIQMISEAARFQYIEGEMRTRIRYNRRSAPDPSVITLENSWGRLST
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(updated)
(first entry)
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    Mismatches

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Pred. No. 2.1e-246;
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Best Local
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Tonge DW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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             421
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                                                                                           LTVQTNIYAVSQGWLPTNNTQPFVTTIVGLYGLCLQANSGQVWIEDCSSEKAEQQWALYA
                                LTVQTNIYAVSQGWLPTNNTQPFVTTIVGLYGLCLQANSGQVWIEDCSSEKAEQQWALYA
                                                                                                                                                                                   NENADVCMDPEPIVRIVGRNGLCVDVRDGRFHNGNAIQLWPCKSNTDANQLWTLKRDNTI 371
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Preproricin is formed in Ricinus communis in the biosynthesis of the ricin toxin. Preproricin is useful on modification giving a materia useful as an antitumour agent without the indiscriminate binding of
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N-PSDB; AAN60193.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                             12 MYAVATWLCFGSTSGWSFTLEDNNIFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGA 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in mrg. ____.

by recombinant
                                                                                                                                                                                                                                    NQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPLEEAISALYYYST
                                                                                                                                                                                                                                                                                                                                           DVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFFPD
AIQESNOGAFASPIQLQRRNGSKFSVYDVSILIPIIALMVYRCAPPPSSQFSLLIRPVVP
                        AIQESNOGAFASPIQLQRRNGSKFSVYDVSILIPIIALMVYRCAPPPSSQFSLLIRPVVP
                                                                                                                                  GGTQLPTLARSFIICIQMISEAARFQYIEGEMRTRIRYNRRSAPDPSVITLENSWGRLST
                                                                                                                                                                                                         NQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPLEEAISALYYYST
                                                                                                                                                                                                                                                                                                                DVRHDIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPD
                                                                                                                                                                                                                                                                                                                                                                                                                    MYAVATWLCFGSTSGWSFTLEDNNIFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGA
                                                                                                    GGTHLPTLARSFIICIQMISEAARFQYIEGEMRTRIRYNRRSAPDPSVITLENSWGRLST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Roberts LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ą,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             84GB-0017915.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85EP-0304711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97.3%;
99.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Atherton KT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 2968; DB 7;
Pred. No. 2.3e-245;
1; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sharpe GS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Windass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Į,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a material
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                 240
                                                                                                                                                     251
                                                                                                                                                                                                                                                                                                                120
                                                                                                                                                                                                                                                                                                                                                                                                                    60
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RESULT 12
AAPPOOD ID AAPPOOD XX

AAPPOOD XX

DT 25-MAPOOD XX

DT 01-NC XX

PI 01-NC XX

Ricir

KW Ricir

KW Ricir

KW Ricir

KW Ricir

KW Ricir

KW Ricir

CXX

RICIR

OX RICIR

PH 15 FOWN

OX MCGII

PT 15 FOWN

OX MCGII

OX RICIR

OX RICIR

OX GILOR

OX CC CIUpda

OX Sequu
                                                                                                                                                                                                  Query Match
Best Local S
Matches 562
                                                                                                                                                                                                                                                                                    to toxins to eliminate cell binding. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                              of DNA from Ricinu communis, Zanibariensis variety. Patent discloses many modifications of ricin in which the lectin binding function of the B chain is diminished or removed, and conjugation
                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; fig 1; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                             Mcdified ricin molecules and toxin conjugates - in which the lectin binding function of the B is removed or diminished to reduce cell binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brown EL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-NOV-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-NOV-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ricinus communis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ricin D; Ricinus mcdified; lectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ricin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003
01-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP90079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAP90079 standard; protein;
                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                         Ricin D (see corresp. AAN90068) found on the EcoRI-HindIII fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAN90068.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GEMY ) GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1989-178366/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    481
 181
                             121
                                                        121
                                                                                                                                                                                                    562;
                                                                                   61
                                                                                                   61 RAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYR 120
                                                                                                                                                         1 MKPGGNTIVIWMYAVATWLCFGSTSGWSFTLEDNNIFPKQYPIINFTTAGATVQSYTNFI
                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGSIRPQQNRDNCLTSDSNIRETVVKILSCGPASSGQRWMFKNDGTILNLYSGLVLDVRA 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDPSLKQIILYPLHGDPNQIWLPLF 565
                                                                                    RAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDPSLKQIILYPLHGDPNQIWLPLF 576
EAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRTRIRYNRRSAPDPSVI
                               AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPLE
                                            AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPLE 180
                                                                                                                                           MKPGGNTIVIWMYAVATWLCFGSTSGWSFTLEDNNIFPKQYPIINFTTAGATVQSYTNFI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jones S;
                                                                                                                                                                                                                                                         562 AA;
                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (updated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87US-0124735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88WO-US04238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           communis; caster beans; Zanibariensis variety;
binding removed; reduced cell binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (caster beans)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entry)
                                                                                                                                                                                                                97.0%;
97.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        562
                                                                                                                                                                                                    0;
                                                                                                                                                                                                                 Score 2960; DB 10;
Pred. No. 1.1e-244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B
                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                               Length 562;
                                                                                                                                                                                                     Indels
                                                                                                                                                                                                    14;
                                                                                                                                                                                                    Gaps
                                                                                      120
                                                                                                                                                                         60
  240
                               180
  Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ф
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Castor bean plant; preproricin; ricin; A chain; B chain; human immunodeficiency virus infection; HIV; toxin; antiretroviral infection; anti-HIV; virucide; viral protease
                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified castor bean preproricin (SEQ ID 10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG78304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAG78304 standard;
                                                                                                                                                             Protein
                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric
                 16-FEB-2000; 2000US-0182759
                                            15-FEB-2001; 2001WO-US05282
                                                                                                     WO200160393-A1
                                                                                                                                                                                        Cleavage-site
                                                                                                                                                                                                                                                                                                                                                 Protein
                                                                          23-AUG-2001
                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                           Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 TLENSWGRLSTAIQESNQGAFASPIQLQRRNGSKFSVYDVSILIPIIALMVYRCAPPPSS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 TLENSWGRLSTAIQESNQGAFASPIQLQRRNGSKFSVYDVSILIPIIALMVYRCAPPPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QFSLLIRPVVPNFNADVCMDPEPIVRIVGRNGLCVDVRDGRFHNGNAIQLWPCKSNTDAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QFSLLIRPVVPNFNADVCMDPEPIVRIVGRNGLCVDVRDGRFHNGNAIQLWPCKSNTDAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EKAEQQWALYADGSIRPQQNRDNCLTSDSNIRETVVKILSCGPASSGQRWMFKNDGTILN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LAATSGNSGTTLTVQTNIYAVSQGWLPTNNTQPFVTTIVGLYGLCLQANSGQVWIEDCSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QLWTLKRDNTIRSNGKCLTTYGYSPGVYVMIYDCNTAATDATRWQIWDNGTIINPRSSLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QLWTLKRDNTIRSNGKCLTTYGYSPGYYVMIYDCNTAATDATRWQIWDNGTIINPRSSLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAATSGNSGTTLTVQTNIYAVSQGWLPTNNTQPFVTTI---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EKAEQQWALYADGSIRPQQNRDNCLTSDSNIRETVVKILSCGPASSGQRWMFKNDGTILN
                                                                                                                                                                                                                                                                                                                                                                                                                                  Ricinus communis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                 /label=
25..565
                                                                                                                                                                                                                   25..291
/label= Ricin_A_chain
/note= "N-glycosidase"
292..303
                                                                                                                                                                                                                                                                           /note= "Proricin consists of the ricin A chain, a linker
    peptide, and the ricin B chain. Proricin is
    proteolytically cleaved between the A chain and
    the linker to yield mature ricin"
                                                                                                                                                               304..565
                                                                                                                                                                                           296..297
                                                                                                                                                                                                                                                                                                                                    /label= Proricin
                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                       /label= Linker_peptide
                                                                                                                                  note=
                                                                                                                                                /label=
                                                                                                                                                                           /label= HIV_protease_cleavage_site
                                                                                                                                                                                                                                                                                                                                                                                                                      immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
                                                                                                                                 "Galactose/N-acetylgalactosamine-binding lectin"
                                                                                                                                                                                                                                                                                                                                                             Signal_peptide
                                                                                                                                                Ricin_B_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                                                                                                                                       type
                                                                                                                                                                                                                                                                                                                                                                                                                                                               protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antiviral agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -VWIEDCSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence relates to the amino acid sequence of a modified preproricin CC protein encoded by AAI64145. The invention relates to a novel toxin CC (e.g. ricin) based antiviral agent which is toxic to virus-infected CC cells, but non-toxic to uninfected cells. The invention has anti-HTV and CC virucide activities. The agent is able to enter all HTV susceptible CC cells, and not just cells known to act as host cells for the virus. The CC antiviral agent remains inert in a cell unless the cell is infected CC with the HTV virus, where the viral protease activates it. Ricin's CC mechanism of action is through inactivation of cellular ribosomes and CC enhancement of binding of the antiviral agent to galactose residues on CC cell surfaces, and its cellular internalisation. The invention is useful CC infections, especially retroviral infections. The antiviral agent is activated in viral particles or early-stage infected cells, killing the CC cells upon infection and effectively preventing the latency/rebound contact in the host genome thereby preventing the latency/rebound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-581908/65
N-PSDB; AAI64145.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 59-63; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BECH-) BECHTEL BWXT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                           361
                                                                                                                                                                                                                                                              301
                                                                                                                                                                                                                                                                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        composition comprising toxin e.g., ricin based antiviral compound for treating viral infections such as human immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                        LTVQTNIYAVSQGWLPTNNTQPFVTTIVGLYGLCLQANSGQVWIEDCSSEKAEQQWALYA 491
                                                                                                                                                                                               RSNGKCLTTYGYSPGVYVMIYDCNTAATDATRWQIWDNGTIINPRSSLVLAATSGNSGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPD 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MYAVATWLCFGSTSGWSFTLEDNNIFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGA 71
DGSIRPQQNRDNCLTSDSNIRETVVKILSCGPASSGQRWMFKNDGTILNLYSGLVLDVRA
                      DGSIRPQQNRDNCLTSDSNIRETVVKILSCGPASSGQRWMFKNDGTILNLYSGLVLDVRA
                                                                                  LTVQTNIYAVSQGWLPTNNTQPFVTTIVGLYGLCLQANSGQVWIEDCSSEKAEQQWALYA
                                                                                                                                                                       RSNGKCLTTYGYSPGVYVMIYDCNTAATDATRWQIWDNGTIINPRSSLVLAATSGNSGTT
                                                                                                                                                                                                                                                         NFNADVCMDPEPIVRIVGRNGLCVDVRDGRFHNGNAIQLWPCKSNTDANQLWTLKRDNTI 360
                                                                                                                                                                                                                                                                               NFNADVCMDPEPIVRIVGRNGLCVDVRDGRFHNGNAIQLWPCKSNTDANQLWTLKRDNTI
                                                                                                                                                                                                                                                                                                                                            AIQESNQGAFASPIQLQRRNGSKFSVYDVSILIPIIALMVYRCAPPPSSQFVSQNYPIVQ
                                                                                                                                                                                                                                                                                                                                                                                    AIQESNQGAFASPIQLQRRNGSKFSVYDVSILIPIIALMVYRCAPPPSSQFSLLIRPVVP 311
                                                                                                                                                                                                                                                                                                                                                                                                                              GGTQLPTLARSFIICIQMISEAARFQYIEGEMRTRIRYNRRSAPDPSVITLENSWGRLST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGTQLPTLARSFIICIQMISEAARFQYIEGEMRTRIRYNRRSAPDPSVITLENSWGRLST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPLEEAISALYYYST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPLEEAISALYYYST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MYAVATWLCFGSTSGWSFTLEDNNIFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   565 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96.6%;
98.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 2947; D. Pred. No. 1.4e 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22;
.4e-243;
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  540
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Matches 482; Query Match

Local

Similarity

83.0%; 89.1%;

Score 2531.5; DB 1 Pred. No. 5.3e-208; Mismatches

DB 18;

Length 540;

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Conservative

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11-JUN-1990;
26-JAN-1995;
07-JUN-1995;
                                                                                                                                      ribosomes and hence preventing protein production. Many different ribosome inhibitory proteins (RIPs) may be produced with an internal linker including maize RIP, Trichosanthin, Ricin A-chain, Abrin-A A-c and Saporin. The RIPs can be used in the construction of therapeutic toxins targeted to specific cells such as tumour cells via the attachment of a targeting polypeptide, e.g., a monoclonal antibody. A further use is in HTV therapy (see US4869903). There is interest in expressing RIP recombinantly in host eukaryotic cells, because of the processing RIP recombinantly in host eukaryotic cells, because of
                                                                     the capacity to provide correct post-translational processing. However, RIPs effectively inhibit protein synthesis in eukaryotic cells resulting in cell death. Since the inactive RIP proteins are not cycloxic to eukaryotic cells, they can be recombinantly expressed in such cells and
                                                                                                                                                                                                                                                                                engineered to contain a selectively removable internal peptide li sequence separating the alpha and beta units. When separated the units regain activity and are capable of inactivating eukaryotic
                                                                                                                                                                                                                                                                                                                    AAW25143 shows a castor oil plant agglutinin protein which was engineered to contain a selectively removable internal peptide
                                                                                                                                                                                                                                                                                                                                                                          Claim 4; Column 121-124; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding pro-ribosome inactivating proteins - precursors of ribosome inactivating proteins; can eukaryotic cells without causing cell death
 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               therapeutic toxin; tumour cell targeted; protein synthesis inhibitor; post-translational modification; cancer; neoplasia; HIV: AIDS; human immunodeficiency virus; acquired immune deficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Castor oil plant agglutinin inactive precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (DOWC ) DOWELANCO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ricin A-chain; Abrin-A A-chain; Saporin; SLT-1; Luffin A; MAP;
Ricinus communis agglutinin; Momordin; PAP-S; Luffin-B; Dianthin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Maize; proRIP; ribosome inactivating protein; alpha; beta subunit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nternal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ď,
                                   converted to active RIP proteins.

ited on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; Protein;
 540 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92US-0987927.
90US-0535636.
95US-0378761.
95US-0485286.
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                                                                                                                                                                                                                                                                                                                      internal peptide linker
                                                                                                                                                                                                                                                                                                                                                                                                                                  be expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                     inactive
                                                                                                                                                                                                                                  Abrin-A A-chain
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RESULT 15
AAW2176
ID 26-SE
XX 25-MA
DT 26-SE
XX DT 26-SE
XX PIO-R
KW DIO-R
KW INACT

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                                                                                                                                                                                                                                                                                                                           pro-Ribosome Inactivating Protein; proRIP; peptide linker; cancer; inactivation; eukaryotic ribosome; alpha fragment; beta fragment; inhibitor; protein synthesis; N-glycosidase; glycosidic bond; liver; rat; ribosomal 28S RNA; cellular proliferation; HIV-infected T cell.
09-DEC-1992;
11-JUN-1990;
                                                                                                                                                                                                                                                                                         Ricinus
                                                                                                                                                                                                                                                                                                                                                                                                                                     R. communis
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26-SEP-1997
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                                                             95US-0378761
                                                                                                                                                                                                                          Location/Qualifiers 152..162
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peptide linker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequences given in AAW21698-710 represent Ribosome Inactivating CC Proteins (RIP's), which may be used in the construction of the protein of the invention. The proRIP has a selectively removable, CC internal peptide linker. The proRIP has a selectively removable, CC internal peptide linker. The precursor sequence is incapable of inactivating eukaryotic ribosomes, but can be converted by removal CC of the linker into a protein having alpha and beta fragments and being CC capable of inactivating eukaryotic ribosomes. RIPs are potent CC inhibitors of eukaryotic protein synthesis. They possess a highly CC specific N-glycosidase activity which cleaves the glycosidic bond of CC adenine 4324 of rat liver ribosomal 28S RNA. RIP's selectively inhibit CC cellular proliferation of cells, e.g. cancer cells and HIV-infected TCC cells. The inactive proRIP proteins make it possible to provide protein CC synthesis inhibitors with uses in practical and improved ways not before CC possible. The RIP can be used to make cycotoxic conjugates.
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Best Local S
Matches 482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Column 119-124; 121pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 89.3 es 482; Conservative
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                                                                                                                                                                                                                                                                                         DVTGEEFFDGNPIQLWPCKSNTDWNQLWTLRKDSTIRSNGKCLTISKSSPRQQVVIYNCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELSNHAELSVTLALDVTNAYVVGCRAGNSAYFFHPDNQEDAEAITHLFTDVQNSFTFAFG
                                                             VKILSCGPASSGQRWMFKNDGTILNLYSGLVLDVRASDPSLKQIILYPLHGDPNQIWLPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  540 AA;
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89.1%;
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Pred. No. 5.3e-208;
6; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English
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Search completed: September 16, 2003, 11:45:15 Job time :  $98.9159~{\rm secs}$ 

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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1: /cgn2_6/ptodata/1,
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3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
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Gapop 10.0 , Gapext 0.5
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           328717 seqs, 42310858 residues
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/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/ABCTUS_COMB.pep:*
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Sequence 14, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 74, Appli
Sequence 74, Appli
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Sequence 27, Appl
Sequence 27, Appl
Patent No. 5248606
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	Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 71, Appli Sequence 71, Appli Sequence 71, Appli Sequence 15, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 7, Appli

#### Sequence 77, Application US/08378761A PATENT NO. 5635384 GENERAL INFORMATION: APPLICANT: WALSH, TERENCE A APPLICANT: HEY, TIMOTHY D APPLICANT: MORGAN, ALICE ER TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE TITLE OF INVENTION: USING NUMBER OF COLUMN STING US-08-378-761A-77 US-08-378-761A-77 Query Match INFORMATION FOR SEQ ID NO: CLASSIFICATION: ATTORNEY/AGENT INFORMATION: NAME: BORUCKI, ANDREA T PATTON NUMBER: 33651 REGISTRATION NUMBER: 33651 REFERENCE/DOCKET NUMBER: 38: TELECOMMUNICATION INFORMATION: TELEPHONE: (317) 337-4846 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/378,761A FILING DATE: 26-JAN-1995 CLASSIFICATION: 435 CLASSIFICATION: 435 MOLECULE TYPE: SEQUENCE CHARACTERISTICS: LENGTH: 540 amino acid COMPUTER READABLE FORM: NUMBER OF SEQUENCES: 8. CORRESPONDENCE ADDRESS: TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear STREET: 9330 ZIONS' CITY: INDIANAPOLIS STATE: IN Match 83.0%; Score 2531.5; DB 1; Local Similarity 89.1%; Pred. No. 1.4e-238; Local Similarity 26; Mismatches 32; COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS MEDIUM TYPE: COUNTRY: ADDRESSEE: 46268 H 540 amino acids E: ANDREA T. BORUCKI 9330 ZIONSVILLE ROAD SU protein Floppy disk 382**7**2B THEREOF, A PROCESS FOR MAKING A METHOD Length 540;

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Matches 482; Conservative

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APPLICANT: HEY, TIMOTHY D

APPLICANT: HEY, TIMOTHY D

APPLICANT: MORGAN, ALICE ER

TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE

TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MA

TITLE OF INVENTION: USING

NUMBER OF SEQUENCES: 81
                          APPLICATION: 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/378761
TITTING DATE: 26-JAN-1995
                                                                                                                                COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                  STREET:
CITY: IN
STATE: I
COUNTRY:
                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                 APPLICATION NUMBER:
REGISTRATION NUMBER:
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               BORUCKI, ANDREA T
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Patent No. 5635384
GENERAL INFORMATION:
APPLICANT: WALSH,
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Best Local
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INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 540 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 38:
TELECOMMUNICATION INFORMATION:
                                                           TITLE OF INVENTION: RIBOSOME-INACTIV
TITLE OF INVENTION: PRECUSOR FORMS
TITLE OF INVENTION: USING
NUMBER OF SEQUENCES: 81
                                                                                                                      APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE ER
                                                CORRESPONDENCE ADDRESS:
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STRANDEDNESS: sin
TOPOLOGY: linear
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                  STREET:
                                  ADDRESSEE:
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                                                                                                                                                                                               Application US/08378761A
                    9330 ZIONSVILLE
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                                ANDREA T. BORUCKI
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89.1%;
                                                                                                           RIBOSOME-INACTIVATING PROTEINS,
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                     ROAD
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Pred. No. 1.4e-238;
""matches 32;
                                                                                        VATING PROTEINS, INACTIVE THEREOF, A PROCESS FOR MA
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US-08-485-286-27

Sequence 27, Application US/08485286

Patent No. 5646026

Patent No. 5646026

Patent No. 5646026

Patent No. 5646026 5646119

GENERAL INFORMATION:
APPLICANT: HEY, TIMOTHY D

APPLICANT: HEY, TIMOTHY D

APPLICANT: MORGAN, ALIGE ER

TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE

TITLE OF INVENTION: USING

NUMBER OF SEQUENCES: 81

NUMBER OF SEQUENCES: 81
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 38:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/378,761A
FILING DATE: 26-JAN-1995
COMPUTER READABLE FORM
                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: US
COUNTRY: US
46268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: protein
                                                             STREET: 9330 ZIONS
               COUNTRY: U
ZIP: 46268
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                                                                                                                                                                                                                                                                                                                                                                                                                                            181
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FRATION NUMBER: 33651
                                                                                                                                                                                                                                                                                                                                                                          GGTQLPTLARSFIICIQMISEAARFQYIEGEMRTRIRYNRRSAPDPSVITLENSWGRLST 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPLEEAISALYYYST 191
                                                                                                                                                                                                                                                                                                                                                                                                                                          GGTQLPTLARSFIICIQMISEAARFQYIEGEMRTRIRYNRRSAPDPSVITLENSWGRLST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPLEEAISALYYYST 180
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99.7%;
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                                                                                                                                                   5248606-4
                                                                                                                                                                                                                                                          ; TITLE OF INVENTION: DNA ENCODING INACTIVE PRECURSOR AND ; ACTIVE FORMS OF MAIZE RIBOSOME INACTIVATIN ; NUMBER OF SEQUENCES: 49
                                                                                                                                                                                     SEQ ID NO:4:
                                                                                                                                                                                                                                                                                                                 ;ALICE E.R.
                                                                                                                                                                                                                                                                                                                                                    ;Patent No.
                                                                                         Query Match 49.0%;
Best Local Similarity 99.7%;
                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 290 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 26-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 382
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                  APPLICANT: WALSH, TERENCE A.; HEY, TIMOTHY D.; MORGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                      FILING DATE: 11-JUN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compati
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
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                                                                                                                                                                    LENGTH: 290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 NQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPLEEAISALYYYST
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290;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MYAVATWLCFGSTSGWSFTLEDNNIFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGA
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                                                                          Conservative
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                                                                        Score 1494.5; DB 6;
Pred. No. 1.1e-137;
0; Mismatches 0;
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Pred. No. 1.1e-137;
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                                                                          Indels
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                                                                                                            Length 290;
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Qy 96 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 155	Qy 36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLENRVGLPINQRFILV 95	Ouery Match 48.6%; Score 1481.5; DB 2; Length 534; Best Local Similarity 72.9%; Pred. No. 5.8e-136; Matches 312; Conservative 26; Mismatches 41; Indels 49; Gaps 11;	; TYPE: amino acid ; TOPOLOSY: linear ; MOLECULE TYPE: protein US-08-356-786-10	: INFORMATION FOR SEQ ID NO: 10:  : SEQUENCE CHARACTERISTICS:  : LENGTH: 534 amino acids	INFORM 1 248-	œ · · ·	PRIOR APPLICATION DATA:  APPLICATION NUMBER: 07/831,967  FILING DATE: 06-FEB-1992	APPLICATION NUMBER: US/08/356,786 FILING DATE: CIASSITETATION: 424	SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:		; COUNTRY: USA ; ZIP: 02109 ; COMPUTER READABLE FORM:	oston Massachusetts	<ul> <li>CORRESPONDENCE ADDRESS:</li> <li>ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, &amp; Thibeault</li> <li>STREET: Exchange Place, 53 State Street</li> </ul>	TION: Bic	; APPLICANT: Oppermann, Hermann ; APPLICANT: Houston, L. L. : APPLICANT: Ring David R	RMATION: Huston, Jar	US-08-356-786-10 ; Sequence 10, Application US/08356786 ; Patent No. 5877305	Db 241 AIQESNQGAFASPIQLQRRNGSKFSVYDVSILIPIIALMYYRCAPPP-SQF 290 RESHIT 6	Qy 252 AIQESNQGAFASPIQLQRRNGSKFSVYDVSILIPIIALMVYRCAPPPSSQF 302	181 GGTQLPTLARSFIICIQMISEAARFQYIEGEMRTRIRYNRRSAPDPSVITLENSWGRLST	Db 121 NQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNIRENIELGNGPLEEAISALYYYST 180  Qy 192 GGTQLPTLARSFIICIQMISEAARFQYIEGEMRTRIRYNRRSAPDDSVITLENSWGRLST 251	132 NOEDAEAITHLFTDVONRYTFAFGGNYDRLEQLAGNLRENIELGNGPLEEAISALYYYST	61 DVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFFPD	Qy 72 DVRHEIPVLPNRVGLDINORFILVELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPD 131
; TYPE: AMINO ACID	TELER: 25-3856 ; TELER: 25-3856 ; INFORMATION FOR SEQ ID NO: 1: ; SEQUENCE CHARACTERISTICS: ; TENGTH: 257-3mino-acids	ERENC		NG DATE: 19920619 SIFICATION: 435 APPLICATION DATA:	AR	; COMPUTER READABLE FORM: ; MEDIUM TYPE: Floppy disk ; COMPUTER: IBM PC compatible	ES.	Tw St		OF INVENTION: Composition and Use for Ribosome SONDERINGS: 57	: APPLICANT: Carroll, Steve F. ; APPLICANT: Lane, Julie A. : "TITLE OF INVENTION: Materials Comprising and Methods of	CANT: Bernhard,		RESULT 7 US-07-901-707-1	Db 409 SGGGSGG 416	Qy 422 AATSGNSG 429	Qy 389 VMIXDCNTAATDATRWQIWDNGTIINPRSSIVI 421	Qy 336 DVRDGREHNGNAIQLWPCKSNTDANQLWTLKRDNIIRSNGKCLTTYGYSPGVY 388 :::   ::   ::     ::     :       :	Db 244 SVYDVSILIPIIALMVYRCAPPPSSQFSLLIRPVVPNFNADVCMDPEIQLV-QSGP 298	276	Oy 216 FQYIESGMRTRIRYNRRSAPDPSVITLENSWGRLSTAIQESNOGAFASPIOLORRNGSKF 275		156 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR	Db 64 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHDDNOEDAEAITHLETDVQNRYTFAFG 123

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RESULT 8
US-07-988-430-1
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                                                                                                                                             APPLICATION NUMBER: US/07/988,430
FILING DATE: 19921209
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bernh
APPLICANT: Bette
APPLICANT: Carro
APPLICANT: Lane,
APPLICANT: Lei,
                                                             APPLICATION NUMBER: US 07/7
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5416202and, Grette
REGISTRATION NUMBER: 35302
                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
            REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Materials Comprising and Methods of TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
STREET:
CITY: Ch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                            STATE: Illinc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
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267; Conserva
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Better, Marc D.
Carroll, Stephen F.
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Pred. No. 9 4e-126;
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US-08-425-336-1
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Matches
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APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
                                                                                                                                 FILING DATA:
CLASSIFICATION: 530
PRIOR APPLICATION NUMBER: 08/064
APPLICATION NUMBER: 12-MAY-193
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                                                                                                                                                                                                                          SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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LENGTH: 267 amino acids
TYPE: AMINO ACID
                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0.
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                          STREET: 6300 S
CITY: Chicago
STATE: Illinoi
                                                                                                                                                                                                                                                                                                                                             ZIP:
                                                                                                             APPLICATION NUMBER: US 07/901,707 FILING DATE: 19-JUN-1992
                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
REFERENCE/DOCKET NUMBER:
               NAME: Meyers, Thomas REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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100.0%; Pred. No. 9.4e-126;
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                                                                            US 07/787,567
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US-08-488-113B-1
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                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxii
TITLE OF INVENTION: Proteins
                                                                       PRIOR APPLICATION DATA:
                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 18-APR-1995
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               PRIOR APPLICATION DATA:
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TYPE: amino acid
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STATE: Illinois
                                   FILING DATE:
                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                   FILING DATE: 07-JUN-1995
                                                                                                                                                                                       APPLICATION NUMBER: US/08/488,113B
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TELEFAX: 312/474-0448
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                       500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                               USA
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                                     12-MAY-1993
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US 07/988,430
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Pred. No. 9.4e-126;
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 5756699
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1,
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TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                             APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxii
TITLE OF INVENTION: Proteins
                                    SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
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REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                      STREET: 500 We CITY: Chicago
                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                    COUNTRY:
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FILING DATE:
                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                ADDRESSEE:
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                                                                                                                                                                                                                                               500 West Madison Street,
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312/707-9155
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07-JUN-1995
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                   US/08/477,484B
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                                                             Version
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amin
                                                       RATERIT NO. 304.7.1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
TITLE OF INVENTION: Proteins
TITLE OF INVENTION: Proteins
                                                                                                                                                                                                                                           Sequence 1, Application US/08646360 Patent No. 5837491
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APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
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TELEFAX: 312/707-9155
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REFERENCE/DOCKET NUMBER: 110
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                                      ADDRESSEE: McAndrews, Held & Malloy, Ltd. STREET: 500 West Madison Street, 34th floor
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Chicago
: Illinois
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TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acids
TYPE: amino acid
TOPOLOGY: lineary
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION UMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
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LENGTH: 267 amino acid
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TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
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APPLICATION NUMBER: US 0
FILING DATE: 19-JUN-1992
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APPLICATION NUMBER: US 0:
FILING DATE: 12-MAY-1993
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Pc1cc-
                                                                                                                                                                                                                                                                                                                                                Local
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 241
                               276 SVYDVSILIPIIALMVYRCAPPPSSQF 302
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SVYDVSILIPIIALMVYRCAPPPSSQF 267
                                                                                                                                                                                                                 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFFHDDNQEDAEAITHLFTDVQNRYTFAFG 155
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                                                                                                                                GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
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100.0%; Pred. No. 9.4e-126;
htive 0; Mismatches 0;
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RESULT 13 US-08-839-765-1

Sequence 1, Application Patent No. 6146631 GENERAL INFORMATION:

Application US/08839765

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APPLICANT:

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US-08-839-765-1
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TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
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LENGTH: 267 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 19-JUN-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 0 FILING DATE: 18-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 11(ILECOMMITUTO TO THE TOTAL TO THE TOTAL TO THE TOTAL TOTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/839,765
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276 SYYDVSILIPIIALMVYRCAPPPSSQF 302
                                                                                                                                                                                                                                                                       156 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISBAAR 215
                                                                                                                                                                                                                                                                                                                                                                                                                                      96 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  267;
                                                                                                                 FQYIEGEMRTRIRYNRRSAPDPSVITLENSWGRLSTAIQESNQGAFASPIQLQRRNGSKF 275
                                                                                                                                                                                                                               GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60661
                                                                     FQYIEGEMRTRIRYNRRSAPDPSVITLENSWGRLSTAIQESNQGAFASPIQLQRRNGSKF 240
                                                                                                                                                                                                                                                                                                                                                                                     ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  45.0%; Score 1372; DB 3; 1
100.0%; Pred. No. 9.4e-126;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US 07/787,567
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US-09-136-389-1
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                                                                                                     Matches
                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                      TELEX: 650 388-1248 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/6
FILING DATE: 13-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
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                                                                                                                   Local
                                                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 32 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/
PTILTING DATE: 12-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/988,430 FILING DATE: 09-DEC-1992
                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 SVYDVSILIPIIALMVYRCAPPPSSQF
                                                                                                   267;
96 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 155
                                                 36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 95
                                                                                                                   Similarity
                                 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           500 West Madison Street, 34th floor
                                                                                                45.0%; Score 1372; DB 3; ilarity 100.0%; Pred. No. 9.4e-126; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                       312/707-9155
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Better, Marc D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IBM PC compatible SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                       312/707-8889
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                                                                                                                                                                                                                                                                                                                                                                                                                           04-NOV-1991
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19-JUN-1992
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                                                                       TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/136,389
FILING DATE: 18-AUG-1998
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
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                                                                                                                                          APPLICANT: Better, marchine Reprint Re
                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 0 FILING DATE: 04-NOV-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 0//301/...
APPLICATION TON 19-30N-1992
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/787,567
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APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
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                                                                                                                                                                                                                                                                                                             NAME: McNicholas, Janet M. REGISTRATION NUMBER: 32,91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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500 West Madison Street, 34th floor
267 amino acids
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Job time : 34.8133 secs
                Search completed: September 16, 2003, 11:51:45
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Best Local Similarity
Matches 267; Conserv
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                                                                                    276 SVYDVSILIPIIALMVYRCAPPPSSQF 302
                                                                  241 SVYDVSILIPIIALMVYRCAPPPSSQF 267
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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Copyright (c) 1993 - 2003 Compuç
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/cgn2_6/ptodata/2/pubpaa//PCTUS_PUBCOMB.pep:*
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US-10-282-935-1
US-09-347-064-10
US-09-347-064-4
US-09-347-935-3
US-09-792-7935-3
US-09-792-793-39
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Sequence 1, Appli
Sequence 10, Appli
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Sequence 3, Appli
Sequence 3, Appli
Sequence 39, Appli
Sequence 6, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 8, Appli
Sequence 2, Appli
Sequence 111, App
Sequence 102, Appli
Sequence 102, Appli
Sequence 251, App
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157.5	159	167.5	184	192	214	216	216	216	246	291	295.5	305.5	321	336	341	343	343	344	344	344	344.5	345	345	345	345	346	347	347	348
	5.2			6.3	7.0	7.1	7.1	7.1	8.1	9.5	9.7	10.0	10.5	11.0	11.2	11.2	11.2	11.3	11.3	11.3	11.3	11.3	11.3	11.3	11.3	11.3	11.4	11.4	11.4
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US-09-770-621-4	US-10-156-761-9724	-10-156	US-10-156-761-14970	US-09-978-274A-8	:-10-074	-10-127-890-	US-09-792-793A-36	-137-077-	US-10-137-077-17	-09-978-	7-	-09	-10-127	-10-127-890-	US-10-127-890-108	US-10-127-890-2	US-09-765-527-247	US-10-127-890-106	US-10-127-890-105	US-10-127-890-100	US-10-127-890-103		-10 - 127	-10-127-	10-127-	27-890	65-5	-10-127	US-10-127-890-4
Sequence 4, Appli		Sequence 10246, A		Sequence 8, Appli	Sequence 5, Appli	Sequence 8, Appli	Sequence 36, Appl	Sequence 18, Appl	Sequence 17, Appl	Sequence 4, Appli	Sequence 9, Appli	'n		100	108	Sequence 2, Appli	247,	Sequence 106, App	105,	100,	e 103,	253,	107,	104,	99,	m .	259,	110	Sequence 4, Appli

## ALIGNMENTS

RESULT 1 US-10-127-890-1

Sequence 1, Application US/10127890 Publication No. US20030166196A1 GENERAL INFORMATION:

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APPLICANT: Hetter, Marc D.
Carroll, Stephen F.
Studnika, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 173
CORRESPONDENCE ADDRESS:
ADDRESSEE: MCANDREWS, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER: EADDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA PPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION NUMBER: US/10/127,890
FILING DATE: 13-MX'-1996
APPLICATION NUMBER: US/10/127,890
FILING DATE: 13-MX'-1996
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MX'-1994
APPLICATION NUMBER: US 07/98/46,360
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 07/98/46,360
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 07/98/46,360
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 07/98/46,361
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/98/430
FILING DATE: 19-MAY-1994
APPLICATION NUMBER: US 07/98/430
FILING DATE: 19-MAY-1996
APPLICATION NUMBER: US 07/98/430
FILING DATE: 19-JUN-1992
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                                                                                                                                         SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 1
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                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/282,935
CURRENT FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: 09/538,873
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/126,826
PRIOR FILING DATE: 1999-03-30
                                                                                                                                                                                                                                                                                                                          APPLICANT: VITTETTA, ELLEN S.
APPLICANT: GHETIE, VICTOR F.
APPLICANT: SMALLSHAW, JOAN
APPLICANT: SALUNA, ROXANA G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS
TITLE OF INVENTION: PROTEINACEOUS COMPOUNDS
FILE REFERENCE: UTSD:884US
                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 23
                   OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1:
                                                                             ORGANISM: Artificial Sequence
                                                           FEATURE:
                                                                                                                     ENGTH:
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NAME: MCNICHOLAS, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
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LENGTH: 267 amino acids
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1 IFPKQYPJINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIDVLPNRVGLPINQRFILV 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVYDVSILIPIIALMVYRCAPPPSSQF 302
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TELEX: 650 388-1248
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100.0%;
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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APPLICANT: Schmidt, Arno
APPLICATION: Album
TITLE OF INVENTION: Album
TITLE OF INVENTION: Album
FILE REFERENCE: 09282-5
CURRENT APPLICATION NUMBER: US/09/347,064A
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: PCT/EP98/00009
EARLIER FILING DATE: 1998-01-02
EARLIER FILING DATE: 1998-01-02
EARLIER FILING DATE: 1998-01-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 26
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Viscum album
                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                       438 IYAVSQGWLPTNNTQPFVTTIVGLYGLCLQANSGQVWIEDCSSEKAEQQWALYADGSIRP 497
                                                                                                                                                                                                                             378 LTTYGYSPGVYVMIYDCNTAATDATRWQIWDNGTIINPRSSLVLAAATSGNSGTTLTVQTN 437
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                                                                                498 QQNRDNCLTSDSNIRETVVKILSCGPASSGQRWMFKNDGTILNLYSGLVLDVRASDPSLK 557
                                                                                                                           125 DYTLGQGWLAGNDTAPREVTIYGFRDLCMESNGGSVWVETCVSSQKNQRWALYGDGSIRP
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RIIIYPATGKPNQMWLPV 262

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GENERAL INFORMATION: CLLEN S.
APPLICANT: VITETTA, ELLEN S.
APPLICANT: VITETTA, ELLEN S.
APPLICANT: GHERIE, VICTOR F.
APPLICANT: GHERIE, VICTOR F.
APPLICANT: SMALLSHAW, JOAN
APPLICANT: BALUNA, ROXANA G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF TITLE OF INVENTION: PROTEINACEOUS COMPOUNDS
FILE REFERENCE: UTSD: 884US
CURRENT APPLICATION NUMBER: US/10/282,935
CURRENT FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: 09/538,873
PRIOR APPLICATION NUMBER: 60/126,826
PRIOR FILING DATE: 1999-03-30
PRIOR FILING DATE: 1999-03-30
PRIOR FILING DATE: 1999-03-30
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US-09-347-064-4
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          NUMBER OF SEQ ID NOS: 23
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TYPE: PRT
ORGANISM: Viscum album
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Similarity 63.2%;
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Pred. No. 1.9e-80;
32; Mismatches 63; Indels
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US-09-792-793A-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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APPLICANT: Coggins, Philip
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
FILE REFERENCE: 25020-601D
CURRENT APPLICATION NUMBER: US/09/792,793A
CURRENT FILING DATE: 2001-02-22
RUMBER OF SEQ ID NOS: 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Trichosanthews kirilowii
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TYPE: PRT
ORGANISM: Abrus precatorius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y Match 13.8%; Score 421; DB 10; Local Similarity 37.3%; Pred. No. 7.5e-33;
                                         171 IGKRV--DKTFLÞSLAIISLENSWSALSKQIQIASTNNGQFESPVVLINAQNQRVTITNV 228
                                                                                   223 MRTRIRYNRRSAPDPSVITLENSWGRLSTAIQ--ESNQGAFASPIQLQRRNGSKFSV--Y 278
                                                                                                                                          116 TAAGKIRENIPLGLPALDSAITTLFYYNAN-----SAASALMYLIQSTSEAARYKFIEQQ 170
                                                                                                                                                                      163 QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICTQMISEAARFQYIEGE 222
279 DVSILIPIIALMVYR 293
                                                                                                                                                                                                                                                                               117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        234 HPTVAVLALMLFVCNPP 250
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                                                                                                                                                                                                                                             59 TISVAIDVTNVYIMGYRAGDTSYFF---NEASATEAAKYVFKDAMRKVTLPYSGNYERLQ
                                                                                                                                                                                                                                                                                                                                                                                         44 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLFNRVGLPINQRFILVELSNHAEL 103
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                                                                                                                                                                                                                                                                                                                                             2 VSFRLSGATSSSYGVFISNLRKALPNERKL-YDIPLL--RSSLPGSQRYALIHLTNYADE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                           60; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10;
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RESULT 7
US-10-127-890-6
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                                                                                                                                                                            Matches
                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEPAX: 312/707-9155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    229 DAGVVTSNIALLLNR 243
                                                    104 SYTLALDYTNAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 162
              59 TISVAIDVTNVYIMGYRAGDTSYFF---NEASATEAAKYVFKDAMRKVTLPYSGNYERLQ 115
                                                                                                                                   44 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 103
                                                                                                                                                                            95;
                                                                                             2 VSFRLSGATSSSYGVFISNLRKALPNERKL-YDIPLL--RSSLPGSQRYALIHLTNYADE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/10/127,890 FILING DATE: 23-Apr-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-UN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                       LENGTH: 247 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/787,567 FILING DATE: 04-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/646,360 FILING DATE: 13-MAY-1996 APPLICATION NUMBER: PCT/US94/05348 FILING DATE: 12-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: McAndrews, Held & Malloy, Ltd.
                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
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                                                                                                                                                                            Conservative
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Carroll, Stephen F.
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                                                                                                                                                                                                 Score 416; DB 12;
Pred. No. 2.3e-32;
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US-10-280-679B-4
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Best Local Similarity
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PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: 07/923,692
PRIOR FILING DATE: 1992-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 07/160,771 PRIOR FILING DATE: 1988-02-26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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    279 DVSILIPIIALMVYR 293
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APPLICANT: Large Scale Biology Corporation
TITLE OF INVENTION: Monopartite RNA Virus Transformation Vectors
FILE REFERENCE: LSBC-0109-US03
CURRENT APPLICATION NUMBER: US/10/280,679B
CURRENT FILING DATE: 2000-10-24
CURRENT FILING DATE: 2000-10-24
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                                                                                                                                                                                                              163 QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 222
                                                                                                                                                                                                                                                                                                                                                         104 SYTLALDYTNAYVYGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 INFTTAGATYQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 103
                                                                                                                                                                                                                                                                                             82 TISVAIDYTNVYIMGYRAGDTSYFF---NEASATEAAKYVFKDAMRKVTLPYSGNYERLQ 138
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IGKRV--DKTFLPSLAIISLENSWSALSKQIQIASTNNGQFETPVVLINAQNQRVMITNV
                                                               MRTRIRYNRRSAPDPSVITLENSWGRLSTAIQ--ESNQGAFASPIQLQRRNGSKFSV--Y 278
                                                                                                                                           TAAGKIRENIPLGLPALDSAITTLFYYNAN-----SAASALMVLIQSTSEAARYKFIEQQ 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-792-793A-34 ; Sequence 34, Application US/09792793A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/09347064A Patent No. US20020045208A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: McDonald, John R.
APPLICANT: Coggins, Philip
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE,
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
FILE REFERENCE: 25020-601D
CURRENT APPLICATION NUMBER: US/09/792,793A
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 93
                                                                                                          SEQ ID NO 8
                                                                                                                 TITLE OF INVENTION: Recombinant Fusion Proteins Based on TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe Viscum TITLE OF INVENTION: album FILE REFERENCE: 09282-5 (CURRENT ENVENTION: Album FILE REFERENCE: 09282-5 (CURRENT APPLICATION NUMBER: US/09/347,064A (CURRENT FILING DATE: 1999-07-02 (EARLIER APPLICATION NUMBER: PCT/EP98/00009 (EARLIER FILING DATE: 1998-01-02 (EARLIER FILING DATE: 1998-01-02 (EARLIER APPLICATION NUMBER: EP 97 10 0012.0 (EARLIER APPLICATION NUMBER: EP 97 10 0012.0 (EARLIER FILING DATE: 1997-01-02 (EARLIER FILING DAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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SEQ ID NO 34
LENGTH: 247
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Eck, Jurgen
APPLICANT: Schmidt, Arno
APPLICANT: Zinke, Holger
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ORGANISM: Viscum album
                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                  ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            223 MRTRIRYNRRSAPDPSVITLENSWGRLSTAIQ--ESNQGAFASPIQLQRRNGSKFSVYDV 280
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                                                                  252
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; ORGANISM: Viscum album US-09-347-064-2
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Patent No. US20020045208A1
GENERAL INFORMATION:
APPLICANT: Eck, Jurgen
APPLICANT: Schmidt, Arno
APPLICANT: Zinke, Holger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver.
SEQ ID NO 2
LENGTH: 252
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Recombinant Fusion Proteins Based on TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe Viscum TITLE OF INVENTION: album FILE REFERENCE: 09282-5 CURRENT APPLICATION NUMBER: US/09/347,064A CURRENT FILING DATE: 1999-07-02
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EARLIER FILING DATE: 1998-01-02
EARLIER APPLICATION NUMBER: EP 97 10 0012.0
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180 YINSGASFLPDVYMLELETSWGQQSTQVQHSTDGVFNNPIRLAIPPGNFVTLTNVRDVIA 239
                                                                                                                                                                166 GNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRT 225
                                                      226 RIRYNRRSAPDPSVITLENSWGRLSTAIQESNQGAFASPIQLQRRNGSKFSVYDVSILIP 285
                                                                                                                124 GH-RDQIPLGIDQLIQSVTALRF---PGGSTRTQARSILILIQMISEAARFNPILWRARQ
                                                                                                                                                                                                                                                               106 TLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               239 SLAIMLFVCGERPS 252
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                                                                                                                                                                                                                             68 TAAIDVTNLYVVAYQAGDQSYFLR-DAPRGAE--THLFTGT-TRSSLPFNGSYPDLERYA 123
                                                                                                                                                                                                                                                                                                                                              10 THQTTGEEYFRFITLLRDYVSSGS-FSNEIPLL-RQSTIPVSDAQRFVLVELTNQGGDSI
                                                                                                                                                                                                                                                                                                                                                                                                 48 TAGATYQSYTNFIRAYRGRLTTGADYRHEIPYLPNRYGLPIN--QRFILYELSNHAELSV 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.4%; Score 379; DB 9; Length 252; 39.5%; Pred. No. 1e-28;
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Pred. No. 4.2e-29;
45; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96; Indels 12;
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RESULT 12
US-10-127-890-111
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-889
TELEPA: 312/707-9155
TELEPA: 650 388-1248
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
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                                                                                                                                                                                       Matches
                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <URKNOWN>
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnika, Gary M.
                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 111:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                           104 SYTLALDYTNAYVYGYRAGNSAYFFH---PDNQEDAEAITHLFTD-VQNRYTFAFGGNYDR 160
63 LAEIAIDVTSVYVVGYQVRNRSYFFKDAPD-----AAYEGLFKNTIKTR--LHFGGSYPS 115
                                                                                                                                    44 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 103
                                                                                                                                                                                    96;
                                                                                           5 VSFSTCGATYITYVNFLNELRVKLKPEGN-SHGIPLLRKKADDP-GKAFVLVALSNDNGQ 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/646,360 FILING DATE: 13-MAY-1996 APPLICATION NUMBER: PCT/US94/05348 FILING DATE: 12-MAY-1994 APPLICATION NUMBER: US 08/064,691 APPLICATION NUMBER: US 08/064,691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 200-70.P4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: McNicholas, Janet M. REGISTRATION NUMBER: 32,918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/10127890 to. US20030166196A1
                                                                                                                                                                                    Conservative
                                                                                                                                                                                                            11.7%;
36.9%;
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                                                                                                                                                                                         45; Mismatches
                                                                                                                                                                                                          Score 358; DB 12;
Pred. No. 1.2e-26;
                                                                                                                                                                                            99;
                                                                                                                                                                                                                                  Length 251;
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US-10-127-890-102
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                                                                         US-10-127-890-102
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Best Local Similarity
                    Query Match
                                                                                                                                                                                                                      TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 102:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Better, Marc D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 312/707-8889
                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161 LEQLAGN--LRENIELGNGPLEEAISALXXXSTGGTQLPTLARSFIICIQMISEAARFQX 218
                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 102:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   231 TAVDQVKPKIALLKFVCKDP 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/646,360
FILING DATE: 13 MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12 MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12 MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/10/127,890 FILING DATE: 23-Apr-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                   NAME: McNicholas, Janet M. REGISTRATION NUMBER: 32,918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 07/787,567 FILING DATE: 04-NOV-1991
                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                      LENGTH: 251 amino acids
                                                                                                                                                                                                                                                                                                    relefax: 312/707-9155
                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 200-70.P4
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Score 354; DB 12;
Pred. No. 2.9e-26;
                          Length 251;
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RESULT 14
US-10-127-890-7
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                             TELEX: 650 388-1248 INFORMATION FOR SEQ ID NO: 7:
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                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
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ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Better, Marc D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        231 TAVDQVKPKIALLKFVCKDP 250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 SYTLALDYTNAYYYGYRAGNSAYFFH--PDNQEDAEAITHLFTD-VQNRYTFAFGGNYDR 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 LAEIAIDVTSVYVVGYQVRNRSYFFKDAPD-----AAYEGLFKNTIKTR--LHFGGSYPS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44 INFTTAGATYQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 103
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                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/988,430 FILING DATE: 09-DEC-1992 APPLICATION NUMBER: US 07/901,707 FILING DATE: 19-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/646,360
FILING DATE: 13 MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12 MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12 MAY-1993
                                                                                                                                            NAME: MCNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/10/127,890 FILING DATE: 23-Apr-2002 CLASSIFICATION: <Unknown>
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STATE: Illinois
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US-09-765-527-251
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                                                                                      TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 251:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/765,527
EILING DATE: 18-Jan-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/621,803
FILING DATE: <Unknown>
                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Methods for Recombinant Microbial Production of Fusion Proteins and BPI-Derived Peptides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170 QIQERA--YRDEVPSLATISLENSWSGLSKQIQLAQGNNGIFRTPIVLVDNKGNRVQITN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               228 VTSKV------VTSNIQLLLNTRNIAEGDNGDV 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            280 VSILIPIIALMVYRCAPPPSSQFSLLI--RPVVPNFNADV 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     222 EMRTRIRYNRRSAPDPSVITLENSWGRLSTAIQ--ESNQGAFASPIQLQRRNGSKFSVYD 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115 QIAAGKPREKIPIGLPALDSAISTLLHYDS-----TAAAGALLVLIQTTAEAARFKYIEQ 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             162 EQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 LSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAE-AITHLFTDVQNRYTFAFGGNYDRL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 KTITVAVDVTNVYIMGYLADTTSYFF---NEPAAELASQYVFRDARRKITLPYSGNYERL 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIP-VLPNRVGLPINQRFILVELSNHAE 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VSFRLSGADPRSYGMFIKDLRNALPFREKV-YNIPLLLPSVSGA---GRYLLMHLFNYDG
                                                                                                                                                                                                                        NAME: Borun, Michael F. REGISTRATION NUMBER: 25,447 REFERENCE/DOCKET NUMBER: 27
                                         TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Chicago
STATE: Illinois
                      TOPOLOGY:
                                                                LENGTH: 332 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun STREET: 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 353.5; DB 1
Pred. No. 3.5e-26;
                                                                                                                                                                                                                                  27129/33199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33; Gaps
```

; SEQUENCE DESCRIPTION: SEQ ID NO: 251: US-09-765-527-251

QV Query Match 11.4%; Score 348.5; DB 9; Length 332; Best Local Similarity 35.0%; Pred. No. 1.6e-25; Matches 104; Conservative 50; Mismatches 118; Indels 25; Gaps

Qγ Вр 

Qy Дb 

дЬ

В Qy 219 IEGEMRTRIRYNRRSAPDPSVITLENSWGRLSTAIQESN-QGAFASPIQLQRRNGSKFSV 277

δÃ

278 YDVSILIPIIALMVYRCAPPPSS----QFSLLIRPVVPNENADVCMDPEPIVRIVGR 330 | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

Search completed: September 16, 2003, 12:09:54 Job time: 60.5688 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

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Result
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Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
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Gapop 10.0 , Gapext 0.5
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           Pred. No. is the number of results predicted by chance to has core greater than or equal to the score of the result being and is derived by analysis of the total score distribution.
      3051
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1 MKPGGNTIVIWMYAVATWLC......KQIILYPLHGDPNQIWLPLF 576
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3: pir3:*
4: pir4:*
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JC5606
JC5032
S23519
PD0018
JT0753
JC4840
JN0108
RLPUGG
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S32430
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RLCSAG
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endo-1,4-beta-xyla rRNA N-glycosidase rRNA N-glycosidase rRNA N-glycosidase xylanase A - Strep rRNA N-glycosidase tritin - wheat rRNA N-glycosidase		,	4	4./	F##. (	
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abrin (clone 3.7)	в39761	N	106	6.4	195.5	) L
rRNA N-glycosidası	T12573	2	289	6.4	967	

## ALIGNMENTS

RESULT 1

A; Molecule type: protein	glycosidase
A; Accession: A03374	gin - beet
A) Reference number: A03374	al protein
0 6 7 6 6	glycosidase
K; Fundasu, G.; Kimura, M.; Funatsu, M. Agric R;ol Chem 43 3221-2224 1970	·qlycosidase
A; Residues: 315-383, 'PS', 386-576 < ARA>	grycosidase grycosidase
A; Molecule type: protein	-glycosidase
A; Accession: A24010	glycosidase
A; Reference number: A24010	b smooth
A: Title: Revised amino moid approximate the province of the p	glycosidase
K;ALGKI, T.; FUDALSU, G.	-qlycosidase
A; Note: this paper cites the others in the series providing experimental details for	TIIN - SMOO
A; Residues: 36-97, 'Q', 99-109, 'S', 111-269, 'D', 272-283, 'L', 285-288, 290-302 < YOS>	cin-B - Tric
A; Molecule type; protein	rin C - Tric
A; Retetence number: AU33/2 A·Accession AU3372	rin - Mongol
A; Title: Isolation and sequences of peptic peptides, and the complete sequence of Ile	(CIONE /.Z)
Agric. Biol. Chem. 42, 1267-1274, 1978	-I B chain -
R; Yoshitake, S.; Funatsu, G.; Funatsu, M.	toe lectin I
A; Cross references: GB:X02388. NTD:G21072 DITM:G3326220 1. DITM:G3326220	inin I precu
A: Residues: 12-75 'n' 77-550 'p' 553-576 'TAN	b precursor
A:MOlecule mana	a precursor
A; Reterior number: A24014; MUID:85179479; PMID:3838723	d precursor
A)TITLE: NUCLEOTIDE sequence of cloned cDNA coding for preproricin.	c precursor
Eur. J. Biochem. 148, 265-270, 1985	rutu brecars
R; Lamb, F.I.; Roberts, L.M.; Lord, J.M.	precursor
A; Cross-references: EMBL: X52908; NID: q21084; PIDN: CAA37095.1: PID: q21085	
A; Residues: 1-576 <tre></tre>	ption
A; Molecule type: DNA	
A; Reterence number: \$20513; MUID:92183016; PMID:1371405 A; Accession: \$20513	
A; Title: The lectin gene family of Ricinus communis: cloning of a functional ricin ge	
Plant Mol. Biol. 18, 515-525, 1992	
R;Tredear J.W.; Roberts I.M.	g printed,
A: XESTOMES: 1-5/6 <hall> A: XESTOMES: 1-5/6 <hall></hall></hall>	ave a
A; Molecule type: DNA	
A; Accession: A24041	
A. Reference number: A24041; MITD: RAGATIA: DATE: 0.00 of a ricin gene from Ricinus communis.	
Nucleic Acids Res. 13, 8019-8033, 1985	
R; Halling, K.C.; Halling, A.C.; Murray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F.	
C;Accessin: A24041; S20513; A24614; A03372; A24010: A03724; S10003	
C:Date: 31-Dec-1003 #secrioror revision 21-Dec-1003 #secrior 1003 #secrioror	
N; CODTAINS: rRNA N-91ycosidase (EC 3.2.2.22)	
ricin D precursor - castor bean	
RLCSD	

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A.Contents: annotation; X-ray crystallography, 2.5 angstroms
C;Comment: The functional molecule is a disulfide-linked dimer of A and B chains, which
C;Comment: The A chain inhibits protein synthesis; it inactivates the 60S ribosomal subu
C;Comment: The A chain; B chains are also responsible for cell agglutination (lecti
C;Comment: This protein is cytotoxic and very poisonous to animals.
C;Comment: This protein is cytotoxic and very poisonous to animals.
C;Comment: This protein is cytotoxic and very poisonous to animals.
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C;Comment: This protein is cytotoxic and very poisonous to animals.
C;Comment: This protein is cytotoxic and very poisonous to animals.
C;Comment: This protein is chain, synthesis; it animals.
C;Comment: This protein is chain,
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A;Title: Structure of ricin B-chain at 2.5 angstrom resolution.
A;Title: Structure of ricin B-chain at 2.5 angstrom resolution.
A;Reference number: A48238; MUID:91352005; PMID:1881882
A;Contents: annotation; X-ray crystallography, 2.5 angstroms
A;Katzin, B.J.; Collins, E.J.; Robertus, J.D.
Proteins 10, 251-259, 1991
A;Title: Structure of ricin A-chain at 2.5 angstroms
A;Reference number: A48239; MUID:91352004; PMID:1881881
A;Reference number: A48239; MUID:91352004; PMID:935404;
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A;Note: this paper, one of a series, summarizes the experimental details for the determing R;Ready, M.P.; Kim, Y.; Robertus, J.D.
Proteins 10, 270-278, 1991
A;Title: Site-directed mutagenesis of ricin A-chain and implications for the mechanism of A;Reference number: A48237; MUID:91352006; PMID:1881883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;212/Active site: Glu #status experimental F;215/Active site: Arg #status predicted F;294-318,334-353,377-394,465-478,504-521/Disulfide bonds: #status experimental F;394-318,334-353,377-394,465-478,504-521/Disulfide bonds: #status experimental F;336,349,360/Binding site: N-acetylgalactosamine (Asp, Asn) #status experimental F;548,569/Binding site: N-acetylgalactosamine (Asp, Asn) #status experimental
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576; Conserv
                                                                                   421 LAATSGNSGTTLTVQTNIYAVSQGWLPTNNTQPFVTTIVGLYGLCLQANSGQVWIEDCSS 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVINAYVVGYR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MKPGGNTIVIWMYAVATWLCFGSTSGWSFTLEDNNIFPKQYPIINETTAGATVQSYTNFI 60
                                                                                                                                                              QLWTLKRDNTIRSNGKCLTTYGYSPGVYVMIYDCNTAATDATRWQIWDNGTIINPRSSLV
                                                                                                                                                                                                 QFSLLIRPVVPNFNADVCMDPEPIVRIVGRNGLCVDVRDGRFHNGNAIQLWPCKSNTDAN 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TLENSWGRLSTAIQESNQGAFASPIQLQRRNGSKFSYYDVSILIPIIALMYYRCAPPPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRTRIRYNRRSAPDPSVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EAISALYYYSTGGTQLPTLARSFIICIQMISEAAREQYIEGEMRTRIRYNRRSAPDPSVI 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MKPGGNTIVIWMYAVATWLCFGSTSGWSFTLEDNNIFPKQYPIINFTTAGATVQSYTNFI 60
           QFSLLIRPVVPNFNADVCMDPEPIVRIVGRNGLCVDVRDGRFHNGNAIQLWPCKSNTDAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLENSWGRLSTAIQESNQGAFASPIQLQRRNGSKFSVYDVSILIPIIALMVYRCAPPPSS 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPLE 180
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Pred. No. 1.7e-224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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A; Cross-references: GB:M12089; NID:g169700; PIDN:AAA33869.1; PID:g169701
A; Archi, T.; Yoshioka, Y.; Funatsu, G.
Biochim. Biophys. Acta 872, 277-285, 1986
A; Title: The complete amino acid sequence of the B-chain of the Ricinus communis aggl
A; Title: The complete amino acid sequence of the B-chain of the Ricinus communis aggl
A; Title: The complete amino acid sequence of the B-chain of the Ricinus communis aggl
A; Title: The complete amino acid sequence of the B-chain of the Ricinus communis aggl
A; Title: The complete amino acid sequence of the B-chain of the Ricinus communis aggl
A; Accession: A24210
A; Reference number: A24210
A; Residues: 303-325, 'F', 327-330, 'T', 332-361, 'D', 363-373, 'G', 375-403, 'T', 405-551, 'V', 5
A; Residues: 303-325, 'F', 327-330, 'T', 332-361, 'D', 363-373, 'G', 375-403, 'T', 405-551, 'V', 5
A; Residues: 303-325, 'F', 327-330, 'T', 332-361, 'D', 363-373, 'G', 375-403, 'T', 405-551, 'V', 5
A; Residues: 303-325, 'F', 327-330, 'T', 332-361, 'D', 363-373, 'G', 375-403, 'T', 405-551, 'V', 5
A; Residues: 303-325, 'F', 327-330, 'T', 332-361, 'D', 363-373, 'G', 375-403, 'T', 405-551, 'V', 5
A; Residues: 303-325, 'F', 327-330, 'T', 332-361, 'D', 363-373, 'G', 375-403, 'T', 405-551, 'V', 5
A; Residues: 303-325, 'F', 327-330, 'T', 332-361, 'D', 363-373, 'G', 375-403, 'T', 405-551, 'V', 5
A; Residues: 303-325, 'F', 327-330, 'T', 332-361, 'D', 363-373, 'G', 375-403, 'T', 405-551, 'V', 5
A; Residues: 303-325, 'F', 327-330, 'T', 332-361, 'D', 363-373, 'G', 375-403, 'T', 405-551, 'V', 5
A; Residues: Aspalating activity and weak cytotoxicity compa
C; Comment: This protein has strong agglutinating activity and weak cytotoxicity compa
C; Comment: This protein has strong agglutinating activity and weak cytotoxicity compa
C; Comment: This protein has strong agglutinating activity and weak cytotoxicity compa
C; Comment: This protein has strong agglutinating activity and weak cytotoxicity compa
C; Comment: This protein has strong agglutinating activity and weak cytoto
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A;Title: The primary sequence of Ricinus communis agglutinin. Comparison with ricin. A;Reference number: A24261; MUID:86059449; PMID:2999130
A;Accession: A24261
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 541 LYSGLVLDVRASDPSLKQIILYPLHGDPNQIWLPLF 576
                                                                                                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      132 NOEDAEAITHLETDVONRYTFAFGGNYDRLEQLAGNLRENIELGNGPLEEAISALYYYST 191
                                                                                                                                                                                                                                                                                                                                    192 GGTQLPTLARSFIICIQMISEAARFQYIEGEMRTRIRYNRRSAPDPSVITLENSWGRLST
                                                                                                          240 AIQESNQGAFASPIQLQRRNGSKFNVYDVSILIPIIALMVYRCAPPPSSQFSLLIRPVVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 MYAVATWLCFGSTSGWSFTLEDNNIFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 DVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAVVVGYRAGNSAYFFHPD 131
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                                                                                                                                                                                                                                                             CGTQIPTLARSFMVCIQMISEAARFQYIEGEMRTRIRYNRRSAPDPSVITLENSWGRLST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DVRHEIPVLPNRVGLPISQRFILVELSNHAELSVTLALDVTNAYVVGCRAGNSAYFFHPD
                                                                                                                                                  AIQESNQGAFASÞIQLQRRNGSKFSVYDVSILIÞIIALMVYRCAÞÞÞSSQFSLLIRÞVVÞ 311
                                                                                                                                                                                                                                                                                                                                                                                                                   NQEDAEAITHLFTDVQNSFTFAFGGNYDRLEQL-GGLRENIELGTGPLEDAISALYYYST
                                   NFNADVCMDPEPIVRIVGRNGLCVDVRDGRFHNGNAIQLWPCKSNTDANQLWTLKRDNTI
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
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   Indels
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of the A-c

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A;Molecule type: protein
A;Residues: 1-69, PS', 72-209, 'A', 211-241, 243-250, 'V', 252-263 <ARA>
A;Residues: 1-69, PS', 72-209, 'A', 211-241, 243-250, 'V', 252-263 <ARA>
A;Residues: 1-69, PS', 72-209, 'A', 211-241, 243-250, 'V', 252-263 <ARA>
A;Experimental source: seed
C;Superfamily: rich; rNA N-glycosidase homology
C;Keywords: duplication; glycoprotein; glycosidase; hydrolase
F;1-63/Product: rich E chain B #status experimental <BCH>
F;1-53/Product: rich E chain B #status experimental <BCH>
F;1-59,60-100,103-141,148-183,187-226,292-63/Region: 40-residue repeats
F;20-39,63-80,151-164,190-207/Disulfide bonds: #status predicted
F;95,135/Binding site: carbohydrate (Asn) (covalent) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ricin E - castor bean (fragment)
N;Contains: chain B; rRNA N-9lycosidase (EC 3.2.2.22) (chain A)
C;Species: Ricinus communis (castor bean)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 20-Aug-1999
C;Accession: S06330; JC5381
R;Laddin, B.F.; Murray, E.E.; Halling, A.C.; Halling, K.C.; Tilakaratne, N.; Long, G.L.;
Plant Mol. Biol. 9, 287-295, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Araki,
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A;Title: Characterization of a cDNA encoding ricin E,
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                                                                                                                                181
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                                                                                                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   315 ADVCMDPEPIVRIVGRNGLCVDVRDGRFHNGNAIQLWPCKSNTDANQLWTLKRDNTIRSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ADVCMDPEPIVRIVGRNGLCVDVRDGRFHNGNAIQLWPCKSNTDANQLWTLKRDNTIRSN
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                                              -SLKQIILYPLHGDPNQIWLPLF 576
                                                                                                                                                                                                                                   QTNIYAVSQGWLPTNNTQPFVTTIVGLYGMCLQANSGKVWLEDCTSEKAEQQWALYADGS
                                                                                                                                                                                                                                                                                  QTNIYAVSQGWLPTNNTQPFVTTIVGLYGLCLQANSGQVWIEDCSSEKAEQQWALYADGS
                                                                                                                                                                                                                                                                                                                                            GKCLTTYGYSPGVYVMIYDCNTAATDATRWQIWDNGTIINPRSSLVLAATSGNSGTTLTV
                                                                                                                                                 IRPQQNRDNCLTSDSNIRETVVKILSCGPASSGQRWMFKNDGTILNLYSGLVLDVRASDP
                                                                                                                       IRPQQNRDNCLTTDANIKGTVVKILSCGPVSSGQRWMFKNDGTILNLYNGLVLDVRRSDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DGSIRPQQNRDNCLTTDANIKGTVVKILSCGPASSGQRWMFKNDGTILNLYNGLVLDVRR 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SDPSLKQIIVHPFHGNLNQIWLPLF 564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SDPSLKQIILYPLHGDPNQIWLPLF 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGSIRPQQNRDNCLTSDSNIRETVVKILSCGPASSGQRWMFKNDGTILNLYSGLVLDVRA 551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LTVQTNIYAVSQGWLPTNNTQPFVTTIVGLYGMCLQANSGKVWLEDCTSEKAEQQWALYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LTVQTNIYAVSQGWLPTNNTQPFVTTIVGLYGLCLQANSGQVWIEDCSSEKABQQWALYA 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NFNADVCMDPEPIVRIVGRNGLCVDVTGEEFFDGNPIQLWPCKSNTDWNQLWTLRKDSTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RSNGKCLTISKSSPRQQVVIYNCSTATVGATRWQIWDNRTIINPRSGLVLAATSGNSGTK 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             911, 191-200, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1341.5; Di
Pred. No. 1e-94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
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C;Comment: Abrin consists of an A chain, which inhibits protein synthesis by inactiva
The A and B chains are linked by a single disulfide bond, which is essential for tox
C;Superfamily: ricin; rRNA N-glycosidase homology
C;Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglutamic a
F;35-285/Product: abrin-c chain A *status predicted <ACH>
F;41-280/Domain: rRNA N-glycosidase homology <RNC>
F;295-562/Product: abrin-c chain B *status predicted <BCH>
F;317-359,360-400,403-441,448-483,487-526,529-562/Region: 40-residue repeats
F;317-359,360-400,403-441,448-483,487-526,529-562/Region: 40-residue repeats
F;318-303,307-330/Binding site: substrate (Tyr, Tyr, Glu, Asn) *status predicted
F;108,147,229,230/Binding site: substrate (Tyr, Tyr, Glu, Asn) *status predicted
F;281-303,320-339,363-380,451-464,490-507/Disulfide bonds: *status predicted
F;324,287,395,435,436/Binding site: Carbohydrate (Asn) (covalent) *status predicted
F;324,287,395,435,436/Binding site: Carbohydrate (Asn) *status predicted
F;324,555/Binding site: N-acetylgalactosamine (Asp, Asn) *status predicted
F;334,555/Binding site: N-acetylgalactosamine (Asp, Asn) *status predicted
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R:Wood, K.A.; Lord, J.M.; Wawrzynczak, E.J.; Piatak, M. Bur. J. Biochem. 198, 723-732, 1991
A:Title: Preproabrin: genomic cloning, characterisation A;Reference number: S16022; MUID:91266957; PMID:2050149
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C:Species: Abrus precatorius (Indian licorice)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999
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A; Residues: 1-562 < WOO>
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           479
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                                                                                                                                                                                                                                                  373 SNGKCLTTYGYSPGVYVMIYDCNTAATDATRWQIWDNGTIINPRSSLVLAATSGNSGTTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                     241
                                                                                                                                                                                                                                                                                                                                            299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 PASASTYLFPGTQ-RYSLRFDGSYGDLERWAHQTREEISLGLQALTHAIS---FLRSGAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 DAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    276;
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GSIRSVQNTNNCLTSKDHKQGSPIVLMACSNGWASQRWLFKNDGSIYNLHDDMVMDVKRS
                                                    GSIRPQQNRDNCLTSDSNIRETVVKILSCGPASSGQRWMFKNDGTILNLYSGLVLDVRAS 552
                                                                                                                                                                                                                                                                                                                                                                                     NADVCMDP-EPIVRIVGRNGLCVDVRDGREHNGNAIQLWPCKSNTDANQLWTLKRDNTIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYQTNIYAVSQGWLPTNNTQPFVTTIVGLYGLCLQANSGQVWIEDCSSEKAEQQWALYAD 492
                                                                                                                                                                                                                        SNGKCLTTEGYAPGNYVMIYDCTSAVAEATYWEIWDNGTIINPKSALVLSAESSSMGGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                             QSVQDTFPNNVILSSINRQPVVVDSLSHPTVAVLALMLFVCNPPNANQSPLLIRSIVE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LCFGSTSGWSfTLEDNNIFP----KQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVR 74
                                                                                                         TVQTNEYLMRQGWRTGNNTSPFVTSISGYSDLCMQAQGSNVWLADCDNNKKEQQWALYTD
                                                                                                                                                                                                                                                                                                                                    ESKICSSRYEPTVRIGGRDGMCVDVYDDGYHNGNRIIAWKCKDRLEENQLWTLKSDKTIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QLPTLARSFIICIQMISEAARFQYIEGEMRTRIRYNRRSAPDPSVITLENSWGRLSTAIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESNQGAFASPIQLQRRNGSKFSVYDVS-ILIPIIALMVYRCAPPPSSQFSLLIRPVVPNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HDIPVLPDPTTVEERNRYITVELSNSERESIEVGIDVTNAYVVAYRAGSQSYFL---RDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43.7%;
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Gaps

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180

240 254

478

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F;1-251/Product: abrin-d chain A #status predicted <ACH>
F;1-260/Domain: rRNA N-glycosidase homology <ARNO-F;246/Domain: rRNA N-glycosidase homology <ARNO-F;261-528/Product: abrin-d chain B #status predicted <BCH>F;283-325,326-366,369-407,414-449,453-492,495-528/Region: 40-residue repeats F;283-325,326-366,369-407,414-499,453-492,495-528/Region: 40-residue repeats F;243,113,195,196/Bsinding site: substrate (Tyr, Tyr, Glu, Asn) *status predicted F;164,157,Active site: Glu, Arg #status predicted F;164,157,Active site: Glu, Arg #status predicted F;200,253,361,401,402/Bsinding site: carbohydrate (Asn) (covalent) *#status predicted F;247-269,286-305,329-346,417-430,456-473/Disulfide bonds: *status predicted F;288,312/Bshding site: N-acetylgalactosamine (Asp, Asn) **status predicted F;500,521/Bsinding site: N
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J. MOl. Biol. 229, 263-267, 1993
A;Title: Primary structure of three distinct isoabrins determined A;Reference number: S32429; MUID:93132798; PMID:8421313
A;Accession: S32431
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N;Contains: rRNA N-glycosidase (EC 3.2.2.22)
C;Species: Abrus precatorius (Indian licorice)
C;Date: 30-Sep-1993 #sequence_revision 01-Aug-1997 *text_change 01-Aug-1997
C;Accession: S32431; S34408
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R;Hung, C.; Lee, M.; Lee, T.; Lin, J.
submitted to the EMBL Data Library, March 1993
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A; Residues: 1-169,'C',171-320,'L',322-528 <HU2>
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A; Accession: S34408
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A; Residues: 1-528 < HUN>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                  172
398 ATDATRWQIWDNGTIINPRSSLVLAATSGNSGTTLTVQTNIYAVSQGWLPTNNTQPFVTT 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 RLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYI 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100 HAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYD 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59 SERESIEVGIDVTNAYVVAYRAGSQSYFL---RDAPASASTYLFPGTQ-RYSLRFDGSYG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40
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                                                                                                                                                                                                                                                                                                                                           VS-ILIPIIALMVYRCAPPPSSQFSLLIRPVVPNFNADVCMDP-EPIVRIVGRNGLCVDV 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSN 99
                                                                                                                                                                   RDGRFHNGNAIQLWPCKSNTDANQLWTLKRDNTIRSNGKCLTTYGYSPGVYVMIYDCNTA 397
                                                                                                                                                                                                                                                                                                                                                                                                                                  {\tt SNRVGVSIRTGTAFQPDPAMLSLENNWDNLSGGVQQSVQDTFPNNVILSSINRQPVVVDS}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGEMRTRIRYNRRSAPDPSVITLENSWGRLSTAIQESNQGAFASPIQLQRRNGSKFSVYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLERWAHQTREEISLGLQALTHAIS---FLRSGASNDEEKARTLIVIIQMASEAARYRYI 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QDQVIKFTTEGATSQSYKQFIEALRQRLTGG--LIHDIPVLPDPTTVEERNRYITVELSN 58
                                                                                      YDDGYHNGNRIIAWKCKDRLEENQLWTLKSDKTIRSNGKCLTTEGYAPGNYVMIYDCTSA
                                                                                                                                                                                                                                                              LSHPTVAVLALMLFVCNPPNANQSPLLIRSIVE -- ESKICSSRYEPTVRIGGRDGMCVDV
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                                                                                                                                                                                                                                                                       289
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A; Residues: 'E', 2-528 <HUN>
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A; Residues: 'E', 2-251 <EVE>
                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 'ME', 2-251 <EV2>
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A; Molecule type: protein
A; Residues: 1-201,203-251 <FUN>
A; Residues: 1-201,203-251 <FUN>
A; Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore,
R; Evensen, G.; Mathiesen, A.; Sundan, A.
J. Biol. Chem. 266, 6848-6852, 1991
A; Title: Direct molecular cloning and expression of two distinct abrin A-chains.
A; Reference number: A39761; MUID:91201329; PMID:2016300
A; Accession: A39761
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C;Date: 31-Dec-1993 #sequence_revision 01-Aug-1997 #text_change 16-Jul-1999
C;Accession: S32429; JT0202; A39761; JC1398; S14472; S24133; S74110; S74111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein
A; Residues: 261-347, '7', 349-351, 'A', 353-357, 'L', 359-528 <KIN>
A; Experimental source: seed
R; Evensen, G.; Mathiesen, A.; Sundan, A.
submitted to the EMBL Data Library, October 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Kimura, M.; Sumizawa, T.; Funatsu, G.
Biosci. Biotechnol. Biochem. 57, 166-169, 1993
A;Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, to A;Reference number: JC1398; MUID:93169023; PMID:7763422
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A;Note: the coding region for the sequence shown is preceded by an ATG codon
A;Note: residues 1-8 were derived from the synthesized primer
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J. Mol. Biol. 229, 263-267, 1993

A;Title: Primary structure of three distinct isoabrins determined by cDNA sequencing.

A;Reference number: S32429; MUID:93132798; PMID:8421313
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                                                                           A;Title: The complete primary structure of abrin-a B chain A;Reference number: S24133; MUID:92371656; PMID:1505674 A;Accession: S24133
                                                                                                                                                                                               A;Cross-references: EMBL:X54873; NID:g16090; PIDN:CAA38655.1; R;Chen, Y.L.; Chow, L.P.; Tsugita, A.; Lin, J.Y. FEBS Lett. 309, 115-118, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Description: Direct molecular cloning of two distinct abrin A-chains. A,Reference number: $14471$ A,Accession: $14472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:X54872
A;Note: residues 1-8 were derived from the synthesized primer
A; Molecule type: protein
A; Residues: 262-297,'Y',299-426,'L',428-466,'P',468-482,'L',484-528 <CHE>
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                                                                                                                                                                                                                                                                                                      PID:g16091
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RESULT 7
S32430
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F;7-261-520/Product: abrin-a chain B #status experimental <BCH>
F;263-325,326-366,369-407,414-449,45-492,495-528/Region: 40-residue repeats F;283-325,326-366,369-407,414-449,45-492,495-528/Region: 40-residue repeats F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental F;74,113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predict F;164,167/Active site: Glu, Arg #status predicted F;247-269,286-305,329-346,417-430,456-473/Disulfide bonds: #status predicted F;288,312/Binding site: N-acetylgalactosamine (Asp, Asn) #status experimental F;561,401/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted F;288,312/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
abrin-b precursor - Indian licorice (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Experimental source: seed C; Comment: Abrin-a is more toxic than ricin. The toxin consists of an A chain, which inttaining receptors on the cell surface. The A and B chains are linked by a single disulficence.
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A; Residues: 262-276, 'X', 278-280; 329-348; 369-388; 399-418
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A; Residues: 89-108; 154-172 <LIN>
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A;Title: Probing the domain structure of abrin-a by tryptic digestion
A;Reference number: S74110; MUID:97008945; PMID:8856055
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 SIEVGIDVTNAYVVAYRAGTQSYFLRDAPSSASD-----YLFTGT-DQHSLPFYGTYGDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            267;
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                                                                                                                                              GCSNGWASQRWVFKNDGSIYSLYDDMVMDVKGSDPSLKQIILWPYTGKPNQIWLTLF 528
                                                                                                                                                                                             SCGPASSGQRWMFKNDGTILNLYSGLVLDVRASDPSLKQIILYPLHGDPNQIWLPLF 576
                                                                                                                                                                                                                                               GYSDLCMQAQGSNVWMADCDSNKKEQQWALYTDGSIRSVQNTNNCLTSKDHKQGSTILLM
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                                                                                                                                                                                                                                                                                                                                               EATYWEIWDNGTIINPKSALVLSAESSSMGGTLTVQTNEYLMRQGWRTGNNTSPFVTSIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GRFHNGNAIQLWPCKSNTDANQLWTLKRDNTIRSNGKCLTTYGYSPGVYVMIYDCNTAAT 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HPTVAVLALMLFVCNPPNANQSPLLIRSIVE--KSKICSSRYEPTVRIGGRDGMCVDVYD
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49.7%; Pred. No. 3.2e-92;
tive 78; Mismatches 175;
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A; Residues: 1-527 < HUN>
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F;7-245/Domain: rRNA N-glycosidase homology cRNG>
F;260-527/Product: abrin-b chain B #status experimental <BCH>
F;280-324,325-365,368-406,413-448,452-491,494-527/Region: 40-residue repeats
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F;74,113,194,195/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F;110,360,400/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;163,166/Active site: Glu, Arg #status predicted
F;287,311/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
F;287,311/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
F;499,520/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
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C:Date: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 20-Aug-1999
C:Accession: S32430; JC1399
R:Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
J. Mol. Biol. 229, 263-267, 1993
A:Title: Primary structure of three distinct isoabrins determined by cDNA series of the primary structure of three distinct isoabrins determined by cDNA series of the primary structure of three distinct isoabrins determined by cDNA series of the primary structure of three distinct isoabrins determined by cDNA series of the primary structure of three distinct isoabrins determined by cDNA series of the primary structure of three distinct isoabrins determined by cDNA series of the primary structure of three distinct isoabrins determined by cDNA series of the primary structure of three distinct isoabrins determined by cDNA series of the primary structure of three distinct isoabrins determined by cDNA series of the primary structure of three distinct isoabrins determined by cDNA series of the primary structure of three distinct isoabrins determined by cDNA series of the primary structure of three distinct isoabrins determined by cDNA series of the primary structure of three distinct isoabrins determined by cDNA series of the primary structure of three distinct isoabrins determined by cDNA series of the primary structure of three distinct isoabrins determined by cDNA series of the primary structure of three distinct isoabrins determined by cDNA series of the primary structure of three distinct isoabrins determined by cDNA series of the primary structure of three distinct isoabrins determined by cDNA series of the primary structure of three distinct isoabrins determined by cDNA series of the primary structure of three distinct isoabrins determined by cDNA series of the primary structure of three distinct isoabrins determined by cDNA series of the primary structure of three distinct isoabrins determined by cDNA series of the primary structure of three distinct isoabrins determined by cDNA seri
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A;Residues: 260-281,'D',283-290,'N',292-349,'PQ',352-377,'N',379-425,'M',427,'D',429-
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Biosci. Biotechnol. Biochem. 57, 166-169, 1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 RLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARPQYI 219
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LMACSNGWASQRWLFRNDGSIYNLHDDMVMDVKRSDPSLKEIILHPYHGKPNQIWLTLF
                                                           VAEATYWEIWDNGTIINPKSALVLSAESSSMGGTLTVQTNEYLMRQGWRTGNNTSPFVTS
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agglutinin I precursor - European elder
;Species: Sambucus nigra (European elder)
C;Species: Sambucus nigra (European elder)
C;Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Aug-1999
C;Accession: $62627; $62619
C;Accession: $62627; $626
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A;Residues: 29-39;309-319 <VA2>
C;Superfamily: ricin; rRNA N-glycosidase homology
E;37-283/Domain: rRNA N-glycosidase homology <RNG>
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A; Residues: 1-570 < VAN>
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A; Accession: $62627
mistletoe lectin I B chain - Viscum album (fragment)
C;Species: Viscum album
C;Date: 03-Jul-1998 #securence rectains to a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S-TGGTQLPTLARSFIICIQMISEAARFQYIEGEMRTRIRYNRRSAPDPSVITLENSWGR 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAVQRD-----NLFVDT-TQEELNFTGNYTSLERQVGFGRVYIPLGPKSLDQAISSLRTY 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N--QEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPLEEAISALYYY 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPD 131
                                                                                                                                                                                                                                                                                                        GTILNLYSGLVLDVRASDPSLKQIILYPLHGDPNQIWL 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GLVLTAPQAAEGTALSLENNIHAARQGW-TVGDVEPLVTFIVGYKQMCIRENGENNEVWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SLVLAATSGNSGTTLTVQTNIYAVSQGWLPTNNTQPFVTTIVGLYGLCLQAN--SGQVWI 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DANQLWTLKRDNTIRSNGKCLTTYGYSPGVYVMIYDCNTAATDATRWQIWDNGTIINPRS 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MSSEIQQAQPGGIFAGVVQLRDERNNSIEVTNFRRLFELTYIAVLLYGCAPVTSSSYSNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LSTAIQESNQGA-FASPIQLQRRNGSKFSVYDVSILIPI--IALMVYRCAPPPSSQFS--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLTAGDTKP-LARGLLVVIQMVSEAARFRYIELRIRTSITDASEFTPDLLMLSMENNWSS 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LYLAVLAICGLGIHG---ALTHPRVTPPVYPSVSFNLTGA--DTYEPFLRALQEKVILGN 62
                                                                                                                                                                                                                                      GTISNPNAKLIMDVAQRDVSLRKIILYRPTGNPNQQWI
                                                                                                                                                                                                                                                                                                                                                                           EDCVLNRVQQEWALYGDGTIRVNSNRSLCVTSEDHEPSDLIVILKC-EGSGNQRWVFNTN
                                                                                                                                                                                                                                                                                                                                                                                                                                          EDCSSEKAEQQWALYADGSIRPQQNRDNCLTSDSNIRETVVKILSCGPASSGQRWMFKND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ECNQLWTFRTDGTIRWLGKCLTA----SSSVMIYDCNTVPPEATKWVVSIDGTITNPHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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      10-Jul-1998 #text_change 07-May-1999
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                                                                                                                                                                                                                                          564
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C;Accession: PD0019
R;Eschenburg, S.; Krauspenhaar, R.; Mikhailov, A.; Stoeva, S.; Betzel, C.; Voelter, Biochen. Biophys. Res. Commun. 247, 367-372, 1998
A;Title: Primary structure and molecular modeling of mistletoe lectin I from Viscum A;Reference number: PD0018; MUID:98308123; PMID:9642133
A;Accession: PD0019
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A;Residues: 1-264 <ESC>
C;Superfamily: ricin; rRNA N-glycosidase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Superfamily: ricin; rRNA N-glycosidase homology
C;Keywords: glycoprotein
F;61,96,136/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Soler, M.H.; Stoeva, S.; Voelter, W.
Blochem. Blophys. Res. Commun. 246, 596-601, 1998
A;Title: Complete amino acid sequence of the B chain of A;Reference number: JW0090; MUID:98289575; PMID:9618256
A;Recession: JW0090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Viscum album (European mistletoe)
C;Date: 18-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 19-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: protein A; Residues: 1-265 < SOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: JW0090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N; Alternate names: ML-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lectin-I B chain - European mistletoe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 166;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                              318 CMDPEPIVRIVGRNGLCVDVRDGRFHNGNAIQLWPCKSNTDANQLWTLKRDNTIRSNGKC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        318 CMDPEPIVRIVGRNGLCVDVRDGRFHNGNAIQLWPCKSNTDANQLWTLKRDNTIRSNGKC 377
                                                  497
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                                                                                                                                                                                                                                                                                                                                                                                                                               166;
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                                                                                                                                                   IYAVSQGWLPTNNTQPFVTTIVGLYGLCLQANSGQVWIEDC-SSEKAEQQWALYADGSIR 496
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                                                                                                       DYTLGQGWLAGNDTAPREVTIYGFRDLCMESNGGSVWVETCDSSQKNQGKWALYGDGSIR 184
                                                                                                                                                                                                                                                                                                                     CSASEPTVRIVGRNGMRVDVRDDDFHDGNQIQLWPSKSNNDPNQLWTIKRDGTIRSNGSC
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PKQNQDQCLTSGRDSVSTVINIVSCSGASGSQRWVFTNEGAILNLKNGLAMDVAQANPKL
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                                                  PQQNRDNCLTSDSNIRETVVKILSCGPASSGQRWMFKNDGTILNLYSGLVLDVRASDPSL
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Pred. No. 1.
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Pred. No. 7.5e-61;
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     244
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N:Contains: rRNA N-glycosiuase (...
C:Species: Abrus precatorius (Indian licorice)
C:Sueris (Indian licorius)
A:Cocession: C:Spfci (Indian licorius)
A:Reference number: A39761; MUID:91201329; PMID:2016300
A:Reference number: A39761; MUID:91201329; PMID:2016300
A:Reference number: DNA
A:Residues: 1-251 CEVE>
A:Reference number: S14471
A:Rocession: Direct molecular cloning of two distinct abrin A-chains.
A:Residues: M' 1-251 CEVE>
A:Reference number: S14471
A:Rocession: S14471
A:Rocessio
                                                                                 rRNA N-glycosidase (EC 3.2.2.2) alpha-trichosanthin precursor [validated] - Mongolian N.Alternate names: alpha-TCS; type I ribosome-inactivating protein C;Species: Trichosanthes kirilowii (Mongolian snake-gourd) C;Date: 30.Sep_1988 #sequence_revision 26-Jan-1996 #text_change 23-Mar-2001 C;Accession: JT0566; A36274; JC1093; A36273; JT0003 R;Shaw, P.C.; Yung, M.H.; Zhu, R.H.; Ho, W.K.K.; Ng, T.B.; Yeung, H.W. Gene 97, 267-272, 1991 A;Reference number: JT0586; MUID:91153657; PMID:1999291
A; Molecule type: mRNA
A; Residues: 1-289 <SH
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                                                                             A; Accession: JT0566
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(Contains: rRNA N-glycosidase (EC 3.2.2.22)
(Species: Abrus precatorius (Indian licorice)
(Date: 21-Feb-1992 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           164 LAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSPIICIQMISEAARFQYIEGEM 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 283 LIPIIALMVYRCAPP 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 SYTLALDYTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQ 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIEVGIDVTNAYVVAYRAGSQSYFL---RDAPASASTYLFTGTQ-RYSLRFDGSYGDLER 118
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                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                         Local
        104 SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE
                                                                                 25 VSFRLSGATSSSYGVFISNLRKALPNERKL-YDIPLL--RSSLPGSQRYALIHLTNYADE
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R;Xiong, J.P.; Xia, Z.X.; Wang, Y.
submitted to the Brookhaven Protein Data Bank, December 1994
A;Reference number: A66711; PDB:ITCS
A;Contents: annotation; X-ray crystallography, 1.7 angstroms, with NADPH, residues 24
R;Xiong, J.P.; Xia, Z.X.; Wang, Y.
Rat. Struct. Biol. 1, 695-700, 1994
A;Title: Crystal structure of trichosanthin-NADPH complex at 1.7 Angstroms resolution A;Reference number: A58622; MUID:95360714; PMID:7634073
A;Contents: annotation; X-ray crystallography, 1.7 angstroms
C;Comment: Alpha-trichosanthin has been used to induce abortions.
                                                                                                                                                                                                                                                                                                                                                                              F;271-289/Domain: carpoxyr-resumence f:271-289/Domain: carpoxyr-resumence f:271-289/D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Description: hydrolyzes the N-glycosiddic bond of a specific adenosine in C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase bomology C;Keywords: abortifacient; glycosidase; hydrolase; root; toxin F;1-23/Domain: signal sequence #status predicted <SIG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 24-270 <COL>
R;Wang, Y.; Qian, R.Q.; Gu, Z.W.; Jin, S.W.; Zhang, L.Q.; Xia,
Pure Appl. Chem. 58, 789-798, 1986
A;Title: Scientific evaluation of Tian Hua Fen (THF): history,
A;Reference number: JT0003
A;Accession: JT0003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;27-266/Domain: rRNA N-glycosidase homology <RNG>
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R;Huang, Q.; Liu, S.; Tang, Y.; Jin, S.; Wang, Y.
submitted to the Brookhaven Protein Data Bank, July 1994
A;Reference number: A67091; PDB:1MRJ
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A;Title: Primary amino acid sequence of alpha-trichosanthin and molecular models for A;Reference number: A36273; MUID:90256789; PMID:2341399
A;Accession: A36273
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A; Residues: 24-56, 'L', 58-59, 'I', 61-71, 'I', 73-81, 85-86, 'L', 88-92, 'DAGLPRNAVL', 93-142, '
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A;Residues: 1-72,'Y',74-90,'S',92-233,'T',235-267,'D',269-289 <ZHE>
A;Cross-references: GB:S70176; NID:g547148; PIDN:AAB31048.1; PID:g5-
A;Cross-references: J.D.; Lopresti, M.; Stone, K.L.; William:
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A;Experimental source: tuber
R;Chow, T.P.; Feldman, R.A.; Lovett, M.; Piatak, M.
J. Biol. Chem. 265, 8670-8674, 1990
A;Title: Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a type I
A;Reference number: A36274; MUID:90256790; PMID:2341400
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A; Residues: 1-233, 'T', 235-246, 'M', 248-289 <CHO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        271-289/Domain: carboxyl-terminal propeptide #status predicted
                                                                                                                                                                                                                                                    Similarity
INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 103
                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                   13.8%; 37.3%;
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                                                                                                                                                                                                                                           Score 421; DB 1;
Pred. No. 1.6e-24;
                                                                                                                                                                  Mismatches
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karasurin - Mongolian snake-gourd
(;Species: Trichosanthes kirilowii (Mongolian snake-gourd)
(;Species: Trichosanthes kirilowii (Mongolian snake-gourd)
C;Date: 30:Sep-1991 #sequence_revision 30:Sep-1991 #text_change 12-Apr-1995
C;Accession: JU0393; pS0163
R;Toyokawa, S.; Takeda, T.; Kato, Y.; Wakabayashi, K.; Ogihara, Y.
Chem. Pharm. Bull. 39, 1244-1249, 1991
A;Title: The complete amino acid sequence of an abortifacient protein, karasa, Title: The complete amino acid sequence of an abortifacient protein, karasa, Reference number: JU0393; MUID:92005921; PMID:1914000
A;Accession: JU0393
                                                                                                   N;Contains: karasurin A
C;Species: Trichosanthes kirilowii var. japonica
C;Species: Trichosanthes kirilowii var. japonica
C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 19-Jul-2002
C;Accession: JC5606; JC5033
R;Mizukami, H.; Iida, K.; Kondo, T.; Ogihara, Y.
Biol. Pharm. Bull. 20, 711-713, 1997
Biol. Pharm. Bull. 20, 711-713, 1997
A;Title: Cloning and bacterial expression of a gene encoding ribosome-inactivating protecting protection of the complex of
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A; molecule type: DNA
A; Residues: 1-289 <MIZ>
A; Cross-references: DDBJ:AB000666; NID:g2329830; PIDN:BAA21786.1; PID:g2329831
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  karasurin C - Trichosanthes kirilowii var. japonica
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DVSILIPIIALMVYR 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IGKRY---DKTFLPSLAIISLENSWSALSKQIQIASTNNGQFETPVVLINAQNQRVTITNV
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                                                                                    163 QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE
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           IAAGKIRENIPLGLPALDSAITTLFYYNAN-----SAASALMVLIQSTSEAARYKFIEQQ
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C;Comment: This protein is a ribosome-inactivating protein and exhibit cytotoxic, abo C;Comment: This protein belongs to type I ribosomal-inactivating proteins which catal C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
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A;Title: Amino acid sequences and ribosome-inactivating activities of karasurin-B and A;Reference number: JC5032; MUID:97108848; PMID:8951169
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R;Kondo, T.; Mizukami, H.; Takeda, T.; Ogihara, Y.
Biol. Pharm. Bull. 19, 1485-1489, 1996
A;Title: Amino acid sequences and ribosome-inactivating A;Reference number: JC5032; MUID:97108848; PMID:8951169
A;Accession: JC5032
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                                                                                                                                                                                                                                                                                                                                     C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology <RNG>F;4-243/Domain: rRNA N-glycosidase homology <RNG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     karasurin-B - Trichosanthes kirilowii var. japonica
C;Species: Trichosanthes kirilowii var. japonica
C;Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;27-266/Domain: rRNA N-glycosidase homology <RNG>
                                                                                                                                                                                                                                                                                                                                                                                 C;Comment: This protein belongs to type I ribosomal-inactivating proteins which C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
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104 SYTLALDYTNAYVYGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 162
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                                                                                                                                       44 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL
                                                                     2 VSFRLSGATSSSYGVFISNLRKALPYERKL-YDIPLL--RSTLPGSQRYALIHLTNYADE
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                                                                                                                                                                                                                   63;
                                                                                                                                                                                                                                                 Score 413; DB 2;
Pred. No. 5.2e-24;
                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                  DB 2;
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Search completed: September 16, 2003, 11:50:32 Job time: 39.3567 secs

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Maximum Match 100%
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P56626 trichosanth
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P2933 momordica b
O03464 phytolacca
P10297 phytolacca
P10297 phytolacca
P23339 phytolacca
P24326 mirabilis j
O40772 phytolacca
P24476 dianthus ca
P24476 dianthus ca
P2759 saponaria o
P20556 saponaria o
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P33185 gelonium mu
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"Primary structure of Ala chain of ricin D."; Agric. Biol. Chem. 43:2221-2224(1979). [6] [6] [CARBOHYDRATE-LINKAGE SITES, AND PARTIAL SEQUENCE. MEDLINE-90344223; PubMed=1368517; Kimura Y., Kusuoku H., Tada M., Takagi S., Funatsu "Structural analyses of sugar chains from ricin A-c Agric. Biol. Chem. 54:157-162(1990). [7] REVIEW. MEDLINE-21480122; PubMed=11595634; Olsnes S., Kozlov J.V.;	SEQUENCE OF 12-576 FROM N.A. MEDLINE-85179479; PubMed=3838723; Lamb A., Roberts L.M., Lord J.M.; "Nucleotide sequence of cloned of Eur. J. Biochem. 148:265-270(1985 [4] SEQUENCE OF 36-302. Yoshitake S., Funatsu G., Funatsu "Isolation and sequences of pepti sequence of Ile chain of ricin-D, Agric. Biol. Chem. 42:1267-1274(1 [5] SEQUENCE OF 315-576. Funatsu G., Kimura M., Funatsu M.	ricin ge ricin ge	SULT 1  RICI_RICCO  RICI_RICCO  STANDARD; PRT; 576 AA.  P02879; P02880;  21-JUL-1986 (Rel. 01, Created)  13-AUG-1987 (Rel. 05, Last sequence update)  15-SEP-2003 (Rel. 42, Last annotation update)  Ricin precursor [Contains: Ricin A chain (rRNA N-g)  (EC 3.2.2.2); Ricin B chain].  Ricinus communis (Castor bean).  Ricinus communis accommunis (Castor bean).  Ricinus communis (Castor bean).  Spermatophyta; Magnoliophyta; embryophyta  Spermatophyta; Magnoliophyta; eudicotyledons; core  eurosids I; Malpighiales; Euphorbiaceae; Ricinus.  [1]  NCBI_TaxID=3988;	34 139.5 4.6 475 1 ABFB_STRLI 35 139 4.6 280 1 RIP1_HORVU 36 138.5 4.5 319 1 SLTA_BP933 37 134.5 4.4 236 1 RIP3_SAPOF 38 133 4.4 548 1 E13B_ARTSP 39 133 4.4 548 1 E13B_ARTSP 40 127 4.2 545 1 AGAL_ASPNG 41 116 3.8 300 1 RIP3_MAIZE 42 115.5 3.8 315 1 SLTA_BPH30 43 114.5 3.8 315 1 SLTA_BPH19 45 114.5 3.8 525 1 SP1_RARFA ALIGNMENTS
G.; hain variant.";	oricin."; complete	, Houston L.L., ine from Ricinus	ycosidase);; Tracheophyta; eudicots; Rosidae;	P96463 streptomyce P22244 hordeum vull P09385 bacteriopha P27560 saponaria o Q59146 arrhrobacte P22222 oerskovia x P28351 aspergillus P25891 zea mays (m P10149 bacteriopha P2852 zea mays (m P08026 bacteriopha Q05308 rarobacter

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Rutenber E., Robertus J.D.; "Structure of ricin B-chain at 2.5-A resolution."; Proteins 10:260-269(1991).
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Katzin B.J., Collins E.J., Robertus J.D.;
"Structure of ricin A-chain at 2.5 A.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS). MEDLINE-87165983; PubMed-3558397;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Day P.J., Ernst S.R., Frankel A.E., Monzingo A.F., Pascal J.M., Molina-Svinth M.C., Robertus J.D.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Structure-based identification of a ricin inhibitor.";
J. Mol. Biol. 266:1043-1049(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Analysis of several key active site residues of ricin A chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97240820; PubMed=9086280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          K-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochemistry 35:11098-11103(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Structure and activity of an active site substitution of ricin A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'X-ray structure of recombinant ricin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biol. Chem. 262:5398-5403(1987).
                                                                                                                                                                                                                                                                                                                                     protein synthesis through the catalytic inactivation of 60S ribosomal subunits. It acts as a glycosidase that removes a specific adenine residue from an exposed loop of 28S ribosomal RNA. As this loop is involved in the binding of elongation factors, the modified ribosomes are unable to support protein synthesis. The A chain can inactivate a few thousand ribosomes per minute, thus inactivating them faster than the cell can make new ones. A single A-chain molecule can therefore kill an animal cell. The B chain binds to cell receptors and facilitates the entry into the cell of the A chain; B chains are also responsible for cell agglutination (Lectin activity). It binds to beta-D-
                 galactopyranoside moieties.

GATALTYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at (CATALTYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at (Specific adenosine on the 28s rrna.

SUBUNIT: Disulfide-linked dimer of A and B chains.

SUBUNIT: Disulfide-linked dimer of A and B chains.

SUBUNIT: Disulfide-linked dimer of A and B chains.

SUBUNIT: The B chain is composed of two domains, each domain consists of 3 homologous subdomains (alpha, beta, gamma).

PTM: THE MAJOR A-CHAIN IS GLYCOSYLATED ONLY IN POSITION 45 AND 'NINGRATIVE IN THE N-TERMINAL SECTION, BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Ricin is higly toxic to animal cells and to a less extent to plant cells. The A chain is responsible for inhib protein synthesis through the catalytic inactivation of 60s protein synthesis through the 60s protein syn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39:1723-1728(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Robertus J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tucker A.D., Thatcher D.R., Derbyshire D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     244:410-422(1994)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ρ.,
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use by non-profit institutions as long amodified and this statement is not removed.
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                                                                                                             ACT_SITE
DISULFID
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                  CONFLICT
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REPEAT
                                                                                                                                                                                                         DOMAIN
                                                                                                                                                                                                                                     CHAIN
PEPTIDE
                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000772; InterPro; IPR001574;
                                                                                                                                                                                                                                                                                                                                                                                                                           PDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                         PROSITE; PS50231; RICIN_B_LECTIN; 2.
PROSITE; PS00275; SHIGA_RICIN; 1.
Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
                                                                                                                                                                                                                                                                                                                                                           GlycoSuiteDB; P02879;
                                              CARBOHYD
                                                                                                                                                                                                                                                                 Glycoprotein;
                                      CARBOHYD
                                                                  CARBOHYD
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                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY: Contains 2 ricin B-type lectin domains.
CAUTION: REF.4 AND REF.5 SEQUENCES HAVE A HIGH NUMBER OF CONFLICTS
WITH THE SEQUENCE TRANSLATED FROM DNA (REF.1, REF.2 AND REF.3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DATABASE: NAME=Protein Spotlight; NOTE=Issue 31 of February 2003;
                                                                                                                                                                                                                                                                                                                                                                     1IL4;
1IL9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WWW-"http://www.expasy.org/spotlight/articles/sptlt031.html"
                                                                                                                                                                                                                                                                                                                                                                                      1BR6;
11L3;
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1IFS;
1IFT;
1IFU;
1RTC;
1OBS;
1OBT;
1BR5;
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1APG;
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A12892;
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X52908;
                                                                                                                                                                                                                                                                                                                       PF00652; Ricin_B_lectin; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                      SM00458; RICIN;
                                                                                                                                                                                                                                                                                                              PR00396;
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CAA37095.1;
CAA26230.1;
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                                                                                                                                                                                                                                                                 Lectin;
                                                                                                                                                                                                                                                                                                                SHIGARICIN.
                                                                                    414
449
497
570
570
212
212
318
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353
353
478
478
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449
76
551
47
                                                                                                                                                                                                                                                                                                                                                   Ricin_B_lectin.
                                                                                                                                                                                                                                                                  Signal;
                    N-LINKED (GLCNAC...).
N-LINKED (GLCNAC...).
E -> D (IN REF. 3).
A -> R (IN REF. 3).
                                                                                                                                                                                                                    RICIN B CHAIN.
RICIN B-TYPE LECTIN
                                                                                                                                                                                                            RICIN B-TYPE LECTIN
                                                                                                                                                                                                                                                RICIN A CHAIN
                                                       N-LINKED (GLCNAC. . .).
/FTId=CAR_000080.
N-LINKED (GLCNAC. . .)
/FTId=CAR_000081.
                                                                                                                                                      2-GAMMA
                                                                                                                                                               2-BETA
                                                                                                                                                                      2-ALPHA
                                                                                                                                                                                          I-BETA.
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Best Local Similarity
                                                                                                                                                                               AGGL_RICCO STANDARD; PRT; 564 AA.

P06750;
01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Agglutinin precursor (Rch.) (Contains: Agglutinin A chain (rRNA flycosidase) (EC 3.2.2.2); Agglutinin B chain].

Ricinus communis (Castor bean).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophy Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Roeurosids I; Malpighiales; Euphorbiaceae; Ricinus.
                                                                                           MEDLINE-86059449; PubMed-2999130;
MEDLINE-86059449; PubMed-2999130;
Roberts L.M., Lamb F.I., Pappin D.J.C., Lo
"The primary sequence of Ricinus communis ricin.";
                                         FISSUE-Seed;
                                                                                                                                                                     NCBI_TaxID=3988;
                                                                             Biol. Chem. 260:15682-15686(1985).
            complete amino acid sequence of the B-chain of the Ricinus
                                                                                                                                                                                                                                                                                                                                                                              541
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    agglutinin isolated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLENSWGRLSTAIQESNQGAFASPIQLQRRNGSKFSVYDVSILIPIIALMVYRCAPPPSS
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                            Yoshioka Y., Funatsu G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAATSGNSGTTLTVQTNIYAVSQGWLPTNNTQPFVTTIVGLYGLCLQANSGQVWIEDCSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EAISALYYYSTGGTQLFTLARSFIICIQMISEAARFQYIEGEMRTRIRYNRRSAPDPSVI
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from large-grain castor
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                                                                                                                   Lord J.M.;
                                                                                                   agglutinin. Comparison with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
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Best Local S
Matches 506
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CHAIN
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GlycoSuiteDB; P06750; -.
InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
Pfam; PF00652; Ricin_B_lectin; 6.
Pfam; PF00161; RIP; 1.
                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                  CARBOHYD
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SMART; SM00458; RICIN; 2.
PROSITE; PS00275; SHIGA_RICIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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RA WOOD K.A., LOTG J.M., WAWEZINGZAK E.J., Platak M.;

RT "Preproabrin: genomic cloning, characterisation and the expression of RT "Preproabrin: genomic cloning, characterisation and the expression of RT the A-chain in Escherichia coli.";

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REC SPECIFIC ACTIVITY: ENGONYELS DETAN.

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01-DEC-1992 (Rel. 24, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Abrin-c precursor (Contains: Abrin-c A chain (rRNA N-glycosidase)
(EC 3.2.22); Abrin-c B chain].
Abrus precatorius (Indian licorice) (Crab's eye).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
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                                                                                           QSVQDTFPNNVILSSINRQPVVVDSLSHPTVAVLALMLFVCNPPNANQSPLLIRSIVE--
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                                                                                                                                                                                                                                                                                                                                     PASASTYLFPGTQ-RYSLRFDGSYGDLERWAHQTREEISLGLQALTHAIS----FLRSGAS
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                                                                                                                                                    ESNQGAFASPIQLQRRNGSKFSVYDVS-ILIPIIALMVYRCAPPPSSQFSLLIRPVVPNF
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4 BY SIMILARITY.
5 ABRIN C A CHAIN (BY SIMILARITY).
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ABRIN C B CHAIN (BY SIMILARITY).
RICIN B-TYPE LECTIN 1.
RICIN B-TYPE LECTIN 2.
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MEDLINE-95333188; PubMed=7608980;

Tahirov T.H., Lu T.-H., Llaw Y.-C., Chen Y.-L., Lin J.-Y.;

Tahirov T.H., Lu T.-H., Llaw Y.-C., Chen Y.-L., Lin J.-Y.;

"Crystal structure of abrin-a at 2.14 A.";

J. Mol. Biol. 250:354-367(1995)

-!- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEINT FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING OF 60S RIBOSC SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 SIBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 SIBBRIN-A IS MORE TOXIC THAN RICIN.

-!- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAN
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P11140; P28589;

01-JUL-1989 (Rel. 11, Created)

11-JUL-1989 (Rel. 29, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)

Abrin-a precursor [Contains: Abrin-a A chain (rRNA N-glycosidase)

Abrin-a precursor [Contains: Abrin-a B chain].

(EC 3.2.22); Abrin-a B chain].

Abrus precatorius (Indian licorice) (Crab's eye).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicottyledons; core eudicots; Rosid:

eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
                                                                                                                                                                                                                                                                                                MEDIJNE-92371656; PubMed=1505674;
MEDIJNE-92371656; PubMed=1505674;
Chen Y.-L., Chow L.-P., Tsugita A., Lin J.-Y.,
"The complete primary structure of abrin-a B chain.";
FEBS Lett. 309:115-118(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "The complete amino acid sequence of the A-chain of protein from the seeds of Abrus precatorius.";

Agric. Biol. Chem. 52:1095-1097(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-251 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=93132798; PubMed=8421313;
Hung C.-H., Lee M.-C., Lee T.C., Lin J.-Y.;
"Primary structure of three distinct isoabrins
sequencing. Conservation and significance.";
                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.14 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A-chains
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91201329; PubMed=2016300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Leaf
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DPSLKEIILHPYHGKPNQIWLTLF 562
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PROSITE; PS50231; RICIN_B_LECTIN;
PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00652; Ricin_B_lectin; Pfam; PF00161; RIP; 1. PRINTS; PR00396; SHIGARICIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDB; 1ABR; 07-FEB-95.
InterPro; IPR000772;
InterPro; IPR001574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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I SUBUNIT: DISULFIDE LINKED DIMER OF A AND B CHAINS.

DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EAC CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GOISMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO TINACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.

SIMILARITY: Contains 2 ricin B-type lectin domains.
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INTERCHAIN (BY SIMILARITY).

BY SIMILARITY.

OLIVER OLIVERON (SILVERON).
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N -> Y (IN REF. 4).
M -> L (IN REF. 4).
T -> P (IN REF. 4).
V -> L (IN REF. 4).
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RICIN B-TYPE LECTIN
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ABRIN-A A CHAIN.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
NCBI_TaxID-3816;
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Q06077; P81374;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
18-FEB-2003 (Rel. 41, Last annotation update)
Abrin-b precursor [Contains: Abrin-b A chain (rRNA N-glycosidase)
Abrin-b B chain].

(EC 3.2.2.22); Abrin-b B chain].
                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE=93132798; PubMed-8421313;

Hung C.-H., Lee M.-C., Lee T.C., Lin J.-Y.;

"Primary structure of three distinct isoabrins determined by cDNA sequencing. Conservation and significance.";

J. Mol. Biol. 229:263-267(1993).
      Kimura M., Sumizawa T., Funatsu G.; "The complete amino acid sequences of the B-chains of abrin-a abrin-b, toxic proteins from the seeds of Abrus precatorius."; Biosci. Biotechnol. Biochem. 57:166-169(1993).
                                                                                                                        MEDLINE=93169023; PubMed=7763422;
                                                                                                                                                      TISSUE=Seed;
                                                                                                                                                                               SEQUENCE OF 260-527.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                           REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00396; SHIGARICIN. SMART; SM00458; RICIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; M98345; AAA32625.1; -.
                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00652; Ricin_B_lectin; Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at specific adenosine on the 28s rnna.

SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.

SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.

DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).

SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.

SIMILARITY: Contains 2 ricin B-type lectin domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: THE A CHAIN IS REPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA. ABRIN-A IS MORE TOXIC THAN RICIN.
FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT FRACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRECEDES ENDOCYTOSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S32430;
                                                                                                                                                                                                                                                                                                                                                                            defense;
                                                                                                                                                                                                                                                                                                                                                                                   PS50231; RICIN_B_LECTIN; PS00275; SHIGA_RICIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                   Lectin;
                                                                                                                                                                                                                                                                                                                                                   Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
Lectin; Pyrrolidone carboxylic acid.
1 250 ABRIN-B A CHAIN.
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H -> W (IN REF. 2).
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H -> W (IN REF. 2).
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2-ALPHA.
2-BETA.
2-GAMMA.
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RICIN B-TYPE LECTIN
RICIN B-TYPE LECTIN
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                           MEDLINE=94003077; PubMed=8400135;
                                       TISSUE-Bark
                                               SEQUENCE OF 26-49 AND 298-321
                                                                                                                MEDLINE=96215449; PubMed=8647092;
                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                     Asteridae;
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                                                                                                        Van Damme E.J.,
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NIGB_SAMNI STANDARD; PRT; 563 AA.

P33183; P33184; P93542;
01-OCT-1993 (Rel. 27, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Rigrin b precursor (Agglutinin V) (SNAV) [Contains: Nigrin b A chailing the Nigrin b B chain].

(rRNA N-glycosidase) (EC 3.2.2.22); Nigrin b B chain].

Sambucus nigra (Buropean elder).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

asteridae. Companyidae. Prices 1910.
Girbes T., Citores L., Ferreras J.M., Rojo M.A., Iglesias Munoz R., Arias F.J., Calonge M., Garcia J.R., Mendez E.; "Isolation and partial characterization of nigrin b, a no
                                                                                                                                                                                                              Van Damme E.J., Barre A., Rouge P., Van Leuven F., Peumans W.J.; "Characterization and molecular cloning of Sambucus nigra agglutinin (nigrin b), a Gallwac-specific type-2 ribosome-inactivating protein from the bark of elderberry (Sambucus nigra)."; "Lur. J. Blochem. 237:505-513(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          469 LMACSNGWASQRWLFRNDGSIYNLHDDMVMDVKRSDPSLKEIILHPYHGKPNQIWLTLF
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Plant Mol. Biol. 22:1181-1186(1993).

-i- FUNCTION: NON-TOXIC TYPE 2 RIP WHICH STRONGLY INHIBITS MAMMALIAN PROTEIN SYNTHESIS BUT DOES NOT AFFECT PLANT NOR BACTERIAL PROTEIN SYNTHESIS. THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION 0F 60S RIBOSOMAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RRNA. THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF NIGRIN B TO THE CELL MEMBRANE THAT PRECEDES
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InterPro; IPR001574; RIP.
Pfam; PF00652; Ricin_B_lectin; 6.
Pfam; PF00161; RIP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00275; SHIGA_RICIN; 1. PROSITE; PS50231; RICIN_B_LECTIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMART; SM00458; RICIN; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
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                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY. SIMILARITY: Contains 2 ricin B-type lectin domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S37382;
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                                                                                                                              VIWMYAVATWLCFGSTSGWSFTLEDNNIFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT
                   TGADVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYRAGNSAYFF
                                                                        MLYFYIVVLAICSVGIQG------IDYPSVSFNLDGAKSATYRDFLSNLRKTVA
                                                                                                                                                                                                                                                                                                                                                Conservative
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NIGRIN B B CHAIN.
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                                                                                                                                                                                                                                   **Soler M.H., Stoeva S., Voelter W.;

**A Soler M.H., Stoeva S., Voelter W.;

**Complete amino acid sequence of the B chain of mistletoe lectin I.";

**Blochem. Biophys. Res. Commun. 246:596-601(1998).

**C: -!- FUNCTION: The A chain is responsible for inhibiting protein synthesis through the catalytic inactivation of 60S ribosomal synthesis through the entry into the cell of the A chain; B chains are also responsible for cell agglutination (lectin activity).

**C: -!- FUNCTION: Disulfide-linked dimer of A and B chains.

-!- SUBUNIT: Disulfide-linked dimer of A and B chains.

-!- SUBUNITION: Due to its immunomodulative effects it is being studied in clinical trials in cancer patients as it may slow the growth of cancer cells and be an effective treatment for solid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MLB_VISAL P81830;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=98289575; PubMed=9618256;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viscum album (European mistletoe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Galactose specific lectin I B chain (MLB) (ML-I B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                            InterPro; IPR000772; Ricin_B_lectin
Pfam; PF00652; Ricin_B_lectin; 6.
                                                                                                                                                            MISCELLANEOUS: Several SIMILARITY: Contains 2
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Best Local S
Matches 166
                                                                                                                                                                                                                          P99184; Q9S8J0;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribosome-inactivating protein bryodin II precursor (rRNA N-
glycosidase) (EC 3.2.2.22) (BDZ).
Bryonia dioica (Red bryony).
Bryonia dioica (Red bryony).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Kosida
eurosids I; Cucurbitales; Cucurbitaceae; Bryonia.
         MEDLINE=95151812; PubMed=7849072; Siegall C.B., Gawlak S.L., Chace
                                                 TISSUE=Root;
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                                                                                                                           Bryonia dioica."
                                                                                                                                                                 Siegall C.
                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                       Patent number US5597569,
                                                                                                                                     Siegall C.B., Gawlak S.L., Marquardt H., "Bryodin 2 a ribosome inactivating protein
                                                                                                                                                                                                                     NCBI_TaxID=3652;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IYAVSQGWLPTNNTQPFVTTIVGLYGLCLQANSGQVWIEDC-SSEKAEQQWALYADGSIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KQIILYPLHGDPNQIWLPLF 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PKQNQDQCLTSGRDSVSTVINIVSCSGASGSQRWVFTNEGAILNLKNGLAMDVAQANPKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DYTLGQGWLAGNDTAPREVTIYGFRDLCMESNGGSVWVETCDSSQKNQGKWALYGDGSIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CSASEPTVRIVGRNGMRVDVRDDDFHDGNQIQLWPSKSNNDPNQLWTIKRDGTIRSNGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS50231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   264 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein;
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                                                                                                       28-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 907.5;
Pred. No. 2e
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GLAM -> SLMV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7D0DC326CCF6F5A4 CRC64;
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       Wolff E.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                            282 AA.
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                                                                                                                                       isolated
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       Mixan
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                                                                                                                                                                                                                                                    eudicots; Rosidae;
                                                                                                                                         from the
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RESULT 9
RIPT_TRIKI
ID RIPT_T
AC P09989
AC P09989
DT 01-WAR
DT 15-SEP
DE RIMOSO
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OS Tricho
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OX NCBI_T
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Best Local
                 RIPT_TRIKI STANDARD; PRT; 289 AA.
P09989;
01-MAR-1989 (Rel. 10, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ribosome-inactivating protein alpha-trichosanthin precursor
(IRNA N-glycosidase) (EC 3.2:2.22) (Alpha-TCS).
Trichosanthes kirilowii (Mongolian snake-gourd).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; Rosideurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00396; SHIGA_RICIN.

PROSITE; PS00275; SHIGA_RICIN; 1.

Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; 134238; -; NOT_ANNO
HSSP; P09989; 1MRJ.
InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Multigene family; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00161; RIP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bioconj. Čhem. 5:423-429(1994).

-!- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS
-!- PROTEIN SYNTHESIS IN ANIMAL CELLS (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bryonia dioica and their utility immunoconjugates.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Marquardt H.; "Characterization of ribosome-inactivating proteins isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE 1 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                            280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 LSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QLAGNL-RENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEG
                                                                                                                                                                                                                                                                                                                                                                                EQRVSENVGTKFKPDPAFLSLQNAWGSLSEQIQIAQTRGGEFARPVELRTVSNTPTFVTN
                                                                                                                                                                                                                                                                                                                                                                                                                EMRTRIRYNRRSAPDPSVITLENSWGRLSTAIQ--ESNQGAFASPIQLQRRNGSKFSVYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESVTVALDVVNVYVVAYRAGNTAYFL---ADASTEANNVLFAGI-NHVRLPYGGNYDGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFSLIGATGATYKTFIRNLRTKLTVGTPRVYDIPVLRNAAAGL---ARFQLVTLTNYNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                282
               Cucurbitales; Cucurbitaceae; Trichosanthes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOT_ANNOTATED_CDS.
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183 B
25 N
30754 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41; Mismatches
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Pred. No. 1.6e-26;
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N-LINKED (GLCNAC. . .) (P
C52BE2F6A873769C CRC64;
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85;

18;

Gaps

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279

136 162 80

Length 282; Indels

(POTENTIAL)

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PARTER PA
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SEQUENCE FROM N.A.
STRAIN-MAXIMOWICZ;
MEDLINE-91153657; PubMed-1999291;
Shaw P.C., Yung M.H., Zhu R.H., Ho W.K.K., Ng T.B., Yeung H.W.;
"Cloning of trichosanthin cDNA and its expression in Escherichia
                                                                                                                                                                                                                       EMBL;
PIR;
                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commentities requires a license agreement (See http://www.jah.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              depurinating mechanism of two ribosome-inactivating proteins.";
Biochem. J. 309:285-298(1995).

-i- FUNCTION: TRICHOSANTHIN IS AN ABORTION-INDUCING PROTEIN. IT IS
CAPABLE OF INHIBITING HIV-1 INPECTION AND REDLICATION. IT
INACTIVATES EUKARYOTIC 60S RIBOSOMAL SUBUNITS.

-i- CAPALTYIC ACTIVITY: Endobydrolysis of the N-glycosidic bond at specific adenosine on the 28S IRNA.

-i- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY TYPE 1 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Collins E.J., Robertus J.D., Lopresti M., Stone K.L., Williams K.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Maximowicz; TISSUE-Tuberous root; MEDLINE-90256789; PubMed=2341399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 24-270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Isolation and DNA sequence of a gene entype I ribosome-inactivating protein."; J. Biol. Chem. 265:8670-8674(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=90256790; PubMed=2341400; Chow T., Feldman R.A., Lovett M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-Maximowicz; TISSUE=Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene 97:267-272(1991).
                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=95344383; PubMed=7619070;
Huang Q., Liu S., Tang Y., Jin S., Wang Y.;
"Studies on crystal structures, active-centre geometry and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Tuberous root;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          models
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Primary amino acid sequence of alpha-trichosanthin and molecular models for abrin A-chain and alpha-trichosanthin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proteins 19:4-13(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       zhou F., Fu 2., Chen M., Lin Y., Pan K.;
"Structure of trichosanthin at 1.88-A resolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=94344957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (-RAY CRYSTALLOGRAPHY (1.88 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pure Appl. Chem. 58:789-798(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  application."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scientific evaluation of Tian Hua Fen (THF): history, chemistry and
                               [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                          1TCS;
                                                                                                                                                                                                                       JT05434; AAA34
                                                                                                                                                                      1MRK;
                                                                                                                                                                                                                                                                              M34858;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hwang K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Qian R.Q., Gu Z.W., Jin S.W., Zhang L.Q., Xia Z.X., Ni C.Z.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chem. 265:8665-8669(1990).
                                                      28-JAN-03.
21-JAN-03.
24-APR-00.
                                                                                                                                       07-FEB-95.
07-FEB-95.
10-JUL-95.
     IPR001574; RIP.
)161; RIP; 1.
                                                                                                                                                                                                                                                       AAA34206.1;
                                                                                                                                                                                                                                                                              AAA34207.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=8066085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Piatak M.;
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STRAND
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                                                                                                                                                                                                      STRAND
TURN
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                                                                                                                         STRAND
          44
25 VSFRLSGATSSSYGVFISNLRKALPNERKL-YDIPLL--RSSLPGSQRYALIHLTNYADE
                     l Similarity
95; Conser
           INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL
                                          202
206
227
231
241
245
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251
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1109
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183
183
82
87
92
143
196
215
231
231
                     Conservative
                                          AA;
                                                     268
31676 MW;
                      60;
                                                                                                                                                                                                                                                                                                              IPLL -> LPLI (IN REF. 4).

MISSING (IN REF. 4).

I -> L (IN REF. 4).

V -> VDAGLPRNAVL (IN REF. 4).

KI -> GL (IN REF. 4).
                                                                                                                                                                                                                                                                               Q -> T (IN REF. 4).
S -> T (IN REF. 2).
MISSING (IN REF. 4).
T -> M (IN REF. 2).
                          Score 421; DB 1
Pred. No. 6e-26;
                                                                                                                                                                                                                                                                                                     K -> S (IN REF. 4).
WS -> LWL (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                               MISSING IN MATURE PROTEIN
                                                                                                                                                                                                                                                                                                                                                    TRICHOSANTHIN
                                                                                                                                                                                                                                                                                                                                                        RIBOSOME-INACTIVATING PROTEIN ALPHA-
                                          5CE09BB630575BB9 CRC64;
                      Mismatches
                                DB 1;
                       82;
                                Length
                      Indels
                       18;
                       Gaps
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                       PIR; JC5606; JC5606.

PIR; JU0393; JU0393.

HSSP; P09989; 1MrJ.

InterPro; IPR001574; RIP.

Pfam; PF00161; RIP; 1.

PRINTS; PR00396; SHIGARICIN.

PROSITE; PS00275; SHIGA_RICIN; 1.

Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                 Toxin; Signal.
                                                                                                                                                                     EMBL; AB000666; BAA21786.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-1992 (Rel. 21, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribosome-inactivating protein karasurin precursor (rRNA N-glycosidase) (EC 3.2.2.22).
Trichosanthes kirilowii (Mongolian snake-gourd).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
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Toyokawa S., Takeda T., Kato Y., Wakabayashi K., Ogihara Y.;
Toyokawa S., Takeda T. Kato Y., Wakabayashi K., Ogihara Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mizukami H., Iida K., Kondo T., Ogihara Y., "Cloning and bacterial expression of a gene encoding inactivating proteins, karasurin-A and karasurin-C, f kirilowii var. japonica.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97356562; PubMed=9212998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 24-270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIPS_TRIKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSUE=Root tuber;
                                                                                                                                                                                                                                                                                                                                        specific adenosine on the 28S TRNA. SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING TYPE 1 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION: ABORTION-INDUCING PROTÉIN. IT INACTIVATES EUKARYOTIC 60S RIBOSOMAL SUBUNITS.
CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
                                                                                                                                                                                                                                                                                                                                                                                                                                          Pharm. Bull. 39:1244-1249(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MRTRIRYNRRSAPDPSVITLENSWGRLSTAIQ--ESNQGAFASPTQLQRRNGSKFSV--Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAAGKIRENIPLGLPALDSAITTLFYYNAN-----SAASALMVLIQSTSEAARYKFIEQQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISVAIDVTNVYIMGYRAGDTSYFF---NEASATEAAKYVFKDAMRKVTLPYSGNYERLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DAGVVTSNIALLLNR 266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DVSILIPIIALMVYR 293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cucurbitales; Cucurbitaceae; Trichosanthes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bull.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20:711-713(1997).
 21
POTENTIAL
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Best Local :
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Viscum album (European mistletoe),
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Santalales; Santalaceae; Viscum.
                                                                                                                                                                       "COmplete amino acid sequence of the A chain of mistletoe lectin I.";
FEBS Lett. 399:133-157(1996).

-i- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN
SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OP 60S RIBOSOMAL
SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNNA. THE
B CHAIN BINDS TO CELL RECEPTORS AND PROBABLY FACILITATES THE ENTRY
INTO THE CELL OF THE A CHAIN; B CHAINS ARE ALSO RESPONSIBLE FOR
CELL AGGLUTINATION (LECTIN ACTIVITY).

-i- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
specific adenosine on the 28S TRNA.

-i- SUBUNIT: Disulfide-linked dimer of A and B Chains.
                            TYPE 2 RIP SUBFAMILY. PIR; PD0018; PD0018.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROPEP
ACT_SITE
SEQUENCE
                                                                                         -!- MISCELLANEOUS: TWO ISOFORMS OF MLA EXIST: GLYCOSYLATED FORM MLA
                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Subsp. album;
MEDLINE=97134581; PubMed=8980141;
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                                                                                                                                                                                                                                                                                                                                                                              Soler M.H., Stoeva S., Schwamborn C., Wilhelm S., Stiefel T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MLA_VISAL
                                                                                                                                                                                                                                                                                                                                                                       Voelter W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P81446;
                                                        SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY
                                                                                                                       PHARMACEUTICAL: Due to its immunomodulative effects it is being studied in clinical trials in cancer patients as it may slow th growth of cancer cells and be an effective treatment for solid
                                                                           AND NON-GLYCOSYLATED
                                                                                                                  tumors
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              289 AA;
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270
289
183
31704
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Pred. No. 2.1e-25;
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KARASURIN-A.
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InterPro; HSSP; P11140;

IPR001574; RIP

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Best Local S
Matches 104
                                                                                                                                                         RIPL_BRYDI STANDARD; PRT; 290 AA.

P33185; Q98819;
01-OCT-1993 (Rel. 27, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribosome-inactivating protein bryodin I precursor (rRNA N-glycosidase)
(EC 3.2.2.2) (BDl).
Bryonia dioica (Red bryony).
Bryonia dioica (Red bryony).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids_I; Cucurbitales; Cucurbitaceae; Bryonia.
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ACT_SITE
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VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00396; SHIGARICIN. PROSITE; PS00275; SHIGA_RICIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARIANT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00161; RIP; 1. PRINTS; PR00396; SHIGA
                                "Molecular, biological, and preliminary structural analysis of recombinant bryodin 1, a ribosome-inactivating protein from th Bryonia dioica.";
                                                                                                                                                                                                                                                                                                                   BRYDI
                                                                          Siegall C.B.;
                                                                                      Gawlak S.L., Neubauer
                                                                                                   MEDLINE=97228081; PubMed=9115985;
                                                                                                                  TISSUE=Leat;
                                                                                                                             SEQUENCE FROM N.A.,
                                                                                                                                                        NCBI_TaxID=3652;
                       Biochemistry 36:3095-3103(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123
                                                                                                                                                                                                                                                                                                                                                                                                                          179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 defense;
                                                                                                                                                                                                                                                                                                                                                                       239 SLAIMLFVCGERPSS
                                                                                                                                                                                                                                                                                                                                                                                                286 IIALMVYRCAPPPSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       104;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRT 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPIN--QRFILVELSNHAELSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GH-RDQIPLGIDQLIQSVTALRF---PGGSTRTQARSILILIQMISEAARENPILWRYRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAAIDVTNAYVVAYQAGDQSYFLR-DAPRGAE--THLFTGT-TRSSLPFNGSYPDLERYA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THQTTGEEYFRFITLLRDYVSSGS-FSNEIPLL-RQSTIPVSDAQRFVLVELTNQGQDSV
                                                                                                                                                                                                                                                                                                                                                                                                                          YINSGASFLPDVYMLELETSWGQQSTQVQHSTDGVFNNPIRLAIPPGNFVTLTNVRDVIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   RIRYNRRSAPDPSVITLENSWGRLSTAIQESNQGAFASPIQLQRRNGSKFSVYDVSILIP 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                               AND X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28478 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.0%;
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                                                                                        Klei H.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OXÍN; Repēat; Glycoprot
BY SIMILARITY.
N-LINKED (GLCNAC.
E -> D (IN MLA').
V -> I (IN MLA').
V -> T (IN MLA').
D -> T (IN MLA').
T -> S (IN MLA').
T -> A (IN MLA').
T -> A (IN MLA').
T -> B (IN MLA').
T -> B (IN MLA').
T -> S (IN MLA').
D -> S (IN MLA').
T -> S (IN MLA').
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 397; DB 1;
Pred. No. 3.9e-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53BAF98D3E0FFE67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                        Chang C.Y.Y., Einspahr H.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein; Lectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                   from the plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. Siegall C.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-95151812; PubMed-7849072; Siegall C.B., Gawlak S.L., Chace D., Wolff E.A., Mixan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent number US5541110, [3]
TURN
STRAND
TURN
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CONFLICT
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ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marquardt H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Root
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 24-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "N-terminal sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Montecucchi P.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=89326691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 24-66.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cloning and expression of a gene encoding bryodin 1 from Bryonia
dioica.";
                                                                                   TURN
STRAND
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HELIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; S16491; S16491.
PDB; 1BRY; 04-MAR-98.
InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Characterization of ribosome-inactivating proteins isolated from
                                                                                                                                          TURN
                                                                                                                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00275; SHIGA_RICIN; 1. plant defense; Protein synthesis_inhibitor; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00396; SHIGARICIN
                                                   STRAND
                                                                                                                        STRAND
                                                                                                                                                                                             STRAND
                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                     3D-structure;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00161; RIP; 1
                                                                     HELIX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BIOTECHNOLOGY: Especially useful as immunotoxin for pharmacological applications as it has low toxicity in rats and mice but is potent once inside target cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Pept.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 equence of some ribosome-inactivating proteins."; Protein Res. 33:263-267(1989).
                                                                                                                                                                                                                                                                                                                                                                     Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=2753596;
Lazzarini A.M., Barbieri L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           their utility as carcinoma-reactive
 23
270
220
2183
2183
214
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214
655
288
311
476
699
799
                                                                                                                                                                                                                                                                                                                                                                     family; Glycoprotein;
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                                                                                                                                                                                                                              N-LINKED (GLCNAC. ..) (POTENTI
N-LINKED (GLCNAC. ..) (POTENTI
E->K: REDUCES ACTIVITY 10-FOLD.
                                                                                                                                                                                                                                                                                                   MISSING IN MATURE PROTEIN.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                      RIBOSOME-INACTIVATING PROTEIN BRYODIN
                                                                                                                                                                                                                LRHXI (IN REF.
                                                                                                                                                                                                                                                                                                                                                                     Signal.
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                                                                                                                                                                                                                                                  (POTENTIAL).
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RESULT 13
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ID RIPG_AC 9318
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Best Local
     Gelonium multiflorum (Euphorbiaceae himalaya).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosid
eurosids I; Malpighiales; Euphorbiaceae; Gelonium.
MCBI_TaxID-3979;
                                                              01-OCT-1993 (Rel. 27, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribosome-inactivating protein gelonin precursor (rRNA N-glycosidase)
(EC 3.2.2.22).
                                                                                                             RIPG_GELMU
P33186;
                                                                                                                                GELMU
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                                                                                                                                                                                   GRLSTAIQ--ESNQGAFASPIQLQRRNGSKFSVYDVS--ILIPIIALMVYR
                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                 SALSKQIQIASTNNGQFESPVVLIDGNNQRVSITNASARVVTSNIALLLNR
                                                                                                                                                                                                                                                                                                  TTGADVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYRAGNSAYF
                                                                                                                                                                                                      YYYTAS-----SAASALLVLIQSTAESARYKFIEQQIGKRV--DKTFLPSLATISLENNW
                                                                                                                                                                                                                       YYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRTRIRYNRRSAPDPSVITLENSW
                                                                                                                                                                                                                                          F---NEASATEAAKFVFKDAKKKVTLPYSGNYERLQTAAGKIRENIPLGLPALDSAITTL
                                                                                                                                                                                                                                                      FHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPLEEAISAL
                                                                                                                                                                                                                                                                                PYERKY-YNIPLL--RSSISGSGRYTLLHLTNYADETISVAVDVTNVYIMGYLAGDVSYF
                                                                                                                                                                                                                                                                                                                     LVLWLLILTIFL-----KSPTVEGD------VSFRLSGATTTSYGVFIKNLREAL 48
                                                                                                                                                                                                                                                                                                                                       IVIWMYAVATWLCFGSTSGWSFTLEDNNIFPKQYPIINFTTAGATVQSYTNFIRAVRGRL
                                                                                                                                                                                                                                                                                                                                                                                               266
290
                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                     12.9%;
                                                                                                                                                                                                                                                                                                                                                                                                   31788 MW;
                                                                                                                                                                                                                                                                                                                                                             67; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     Score 393; DB 1; Length 290; Pred. No. 9.8e-24;
                                                                                                                                                                                                                                                                                                                                                                                                E966CD9C031A42DB CRC64;
                                                                                                                     316
                                                                                                                     A
                                                                                                                                                                                                                                                                                                                                                            92;
                       core eudicots; Rosidae;
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Best Local Sin
Matches 116;
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CONFLICT
CONFLICT
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                 PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                              Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS00275; SHIGA_RICIN; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00396; SHIGARICIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00161; RIP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; JT0753; JT0753.
HSSP; P09989; 1MRJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; L12243; AAA16312.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 specific adenosine on the 28S rnna.
-!- SUBUNIT: Homodimer.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lappi D.;
"N-terminal sequence of some ribosome-inactivating proteins.";
"nt. J. Pept. Protein Res. 33:263-267(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDLINE=94085781; PubMed=7916721;

Nolan P.A., Garrison D.A., Better M.;

"Cloning and expression of a gene encoding gelonin, a ribosome-
inactivating protein from Gelonium multiflorum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hosur M.V., Nair B., Satyamurthy P., Misquith S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS). MEDLINE=95333189; PubMed=7608981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inactivating protein fro
Gene 134:223-227(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Mol. Biol. 250:368-380(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Montecucchi P.C., Lazzarini A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 47-93.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "X-ray structure of gelonin at 1.8-A resolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kannan K.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=89326691; PubMed=2753596;
                                                                                                                                                                                                                                                                                                                                                                                                                                          lant defense;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE 1 RIP SUBFAMILY
                   171
                                                121
                                                                            116
                                                                                                       63
                                                                                                                                                                                     5 GNTIVIWM-YAVATWLC-----FGSTSG-WSFTLEDNNIFPKQYPI--INFTTAGATVQS
                                                                                                                                                                                                                                    Similarity
             NIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRTRIRYN
                                         VVGYQVRNRSYFFKDAPD-----AAYEGLFKNTIKTR--LHFGGSYPSLE----GEKAYRE
                                                                    VVGYRAGNSAYFFH--PDNQEDAEAITHLFTD-VQNRYTFAFGGNYDRLEQLAGN--LRE 170
                                                                                                                            YTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAY
                                                                                                   YVNFLNELRVKLKPEGN-SHGIPLLRKKCDDP-GKCFVLVALSNDNGQLAEIAIDVTSVY
                                                                                                                                                           GNMKVYWIKIAVATWFCCTTIVLGSTARIFSLPTNDEEETSKTLGLDTVSFSTKGATYIT
                                                                                                                                                                                                                                                                               316
                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                               ΑĄ;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein synthesis inhibitor; Hydrolase; Toxin; Signal;
                                                                                                                                                                                                                                                                                            26
46
297
316
316
235
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212
90
                                                                                                                                                                                                                                                                             35418 MW;
                                                                                                                                                                                                                                 12.7%;
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Pred. No. 3.9e-23;
                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. . .).
                                                                                                                                                                                                                                                                                                                                                                   MISSING
                                                                                                                                                                                                                                                                                                                                                                               RIBOSOME-INACTIVATING PROTEIN GELONIN
                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL
                                                                                                                                                                                                                                                                          -> K (IN REF. 2).
-> D (IN REF. 2).
1252F3E710901B85
                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                 IN MATURE
:: :: :: :: :: :: :: ::
                                                                                                                                                                                                                                                                                                                                                                 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stirpe F., Soria
                                                                                                                                                                                                                                               Length 316;
                                                                                                                                                                                                                                                                               CRC64;
                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Surolia
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cucumis figarei.
Cucumis figarei.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
Spermatophyta; Magnoliophyta; Cucumbitaceae; Cucumis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no ways modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Putative ribosome-inactivating protein precursor (rRNA N-glycosidase)
                                                                                                                                                                                                                                                                                     ACT_S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ÷
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yamada T., Ohki S.T., Osaki T.;
"Cloning and analysis of a cDNA coding a putative ribosome:
"Cloning and analysis of a cDNA coding a putative ribosome:
inactivating protein from Cucumis figarei.";
Plant Biotechnol. 17:337-340(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=131071;
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EC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIP1_CUCFI
                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                        CARBOHYD
                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                   SIGNAL
                                                                                                                                                                                                                                                                                                                                              Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB045560; BAB19677.1;
                                                                                                                                                                                                                                                                                                                                 Toxin; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at a specific adenosine on the 28S rRNA. SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE 1 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                     _SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    171
 163 QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE
                                                                                                                                                                                                                                                                                                                                                                                               PF00161;
                                                               103
                                                                                                                                                                                                                                                                                                                                                                                                                            P16094;
                                84
                                                                                                                         44 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVL-PNRVGLPINQRFILVELSNHAE
                                                                                                                                                            86;
                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LKFVDKDPKT---SLAAELIIQNYESLVGFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QRIRPANNTISLENKWGKLSFQIRTSGANGMESEAVELERANGKKYYVTAVDQVKPKIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RRSAPDPSVITLENSWGRLSTAIQESN-QGAFASPIQLQRRNGSKFSVYDVSILIPIIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MYYRCAPPPSSQFSLLIRPVVPNFNADVCMD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTFIENQIRN--NFQ
                                                            LSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLE
                                                                                            VKFSLLGSNHKSYSKFITSMRNALPNAGDI-YNIPLLVPSISG---SRRYILMQLSNYEG
                                {\tt NTITMAVDVTNVYIMGYLVNGTSYFF---NETDAQLASKFVFQGTKSITLPYSGNYQKLQ}
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22
185
103
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252
286
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                                                                                                                                                            Conservative
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286
185
103
110
252
                                                                                                                                                                                                                         31771 MW;
                                                                                                                                                                          12.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                            56;
                                                                                                                                                                                                                                      PUTATIVE RIBOSOME-INACTIVATING PROTEIN
BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                          Score 375.5;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                    POTENTIAL.
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                                                                                                                                                                                                                        4EFD4966E604DA41 CRC64;
                                                                                                                                                            Mismatches
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                                                                                                                                                                            2.3e-22;
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                                                                                                                                                                                          DB 1;
                                                                                                                                                            85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       core eudicots;
                                                                                                                                                                                          Length 286;
                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tracheophyta;
                                                                                                                                                               17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosidae;
                                                                                                                                                               Gaps
                                                                  162
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RESULT 15
RIPB_LUFCY
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Matches
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01-AUG-1991 (Rel. 19, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribosome-inactivating protein luffin-B (rRNA)
(EC 3.2.2.22)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryor
Spermatophyta; Magnoliophyta; eudicotyledons; c
eurosids I; Cucurbitales; Cucurbitaceae; Luffa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Islam M.R., Hirayama H., Funatsu G.;

"Complete amino acid sequence of luffin-b, a ribosome-inactivating protein from sponge gourd (Luffa cylindrica) seeds.";

Agric. Biol. Chem. 55:229-238(1991).

-I- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at specific adenosine on the 28S IRNA.

-I- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; JN0108; JN0108.
HSSP; P16094; 1AHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Luffa cylindrica (Smooth loofah) (Sponge gourd).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RIPB_LUFCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE 1 RIP SUBFAMILY.
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                                                                                                           172
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                                                                                                                                                                                                                                                                                                                                                                                 SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                       VSFSLSGADSKSYSKFITALRKALPSKEKVSNIPLLLPSASGA---SRYILMQLSNYDAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFTTAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINORFILVELSNHAEL
  ASKVQI 235
                                                                                                                                                                                                                                                                                                                              AITMAIDVTNVYIMGYLVNSTSYF---ANESDAKLASQYVFKGSTLVTIPYSGNYERLQN 116
                                                        SILIPI 286
                                                                                                           IERIPKN--EVPSPAALSLENEAWSLLSKQIQLAQTNNGAFRTPVVIIDNKGQRVEITNL
                                                                                                                                                           RTRIRYNRRSAPDPSVITLEN-SWGRLSTAIQ--ESNQGAFASPIQLQRRNGSKFSVYDV
                                                                                                                                                                                                                   AAGKIREKIPLGFRALDSALTSIFHYDS----TAAAAAFLVILQTTAEASRFKYIEGQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160
250 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 I
27293 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12.1%; 32.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 369; DB 1;
Pred. No. 6.2e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F01A8DC8A1078700 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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Search completed: September 16, 2003, 11:46:01 Job time : 22.1928 secs

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## ALIGNMENTS

RESULT 1
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DT PRINTS; PR00396; SHIGARICIN.
SMART; SM00458; RICIN; 2.
PROSITE; PS50231; RICIN, BLECTIN; 2.
PROSITE; PS00275; SHIGA\_RICIN; 1.
PROSITE; PS00338; SOMATOTROPIN\_2; 1. Roberts L.M., Tregear J.W., Lord J.M.;

"Molecular cloning of ricin";

"Molecular cloning of ricin";

Targeted Diagn. Ther. 7:81-97(1992).

-i- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 28S RRNA.

-i- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

EMBL; \$40366; AAB22582.1;

HSSP; P02879; 1BR6. Q41174 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Mapighiales; Euphorbiaceae; Ricinus. 01-NOV-1996 (TERMBLrel. 01, Created)
01-NOV-1996 (TERMBLrel. 01, Last sequence update)
01-MAR-2003 (TERMBLrel. 23, Last annotation update)
Proricin A chain (EC 3.2.2.22) (rRNA N-glycosidase) SEQUENCE Pfam; PF00652; Ricin\_B\_lectin; Pfam; PF00161; RIP; 1. InterPro; IPR000772; Ricin\_B\_lectin.
InterPro; IPR001574; RIP.
InterPro; IPR001594; RIP.
InterPro; IPR001400; Somatotropin.
Pfam; PF00652; Ricin\_B\_lectin; 6. SEQUENCE FROM N.A. MEDLINE=92338377; PubMed=1633311; Hydrolase; NCBI\_TaxID=3988; Ricinus communis (Castor bean) (Fragment). 541 AA; Toxin. PRELIMINARY; 60281 MW; PRT; 2B7B2CDEF1F2E9D9 CRC64; 541 δ

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Matches 539
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Type 2 ribosome-inactivating protein cinnamomin III pr
EC 3.2.22) (TRNA N-91ycosidase).
EC 3.2.22) (TRNA N-91ycosidase).
Cinnamomum camphora (Camphor tree).
ELMATYOTA; Viridiplantae; Streptophyta; Embryophyta; T
Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cin
NCBI_TaxID=13429;
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

Yang Q., Gong Z.Z., Liu W.Y.;

Molecular cloning of three type 2 RIP (ribosome-inactivating genes encoding cinnamomin proteins and study of their expressions)
                                                -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING EMBL; AY039803; AAK82460.1; .
InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
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Pred. No. 7.8e-224;
1; Mismatches 1;
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                                                                                                                                                                 094BW4.
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Type 2 ribosome-inactivating protein cinnamomin II pre
EC 3.2.22) (TRNA w-glycosidase).
Cinnamomum camphora (Camphor tree).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; T
Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cin
NCBL_TaxID=13429;
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SMART; SM00458; RICIN; 2.
PROSITE; PS50231; RICIN_B_LECTIN;
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SIGNAL 1 32
                                                        SEQUENCE FROM N.A.
Yang Q., Gong Z.Z., Liu W.Y.;
"Molecular cloning of three type 2 RIP
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TYPE 2 RIBOSOME-INACTIVATING PROTEIN
CINNAMOMIN III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1492;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      940D10F01E7FB558 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                    and
                                                                                                                                                                                                                                                                                                                                                                                                                                                   580
                                    (ribosome-inactivating pr
study of their expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; DB 10;
?.6e-113;
                                                                                                                                                                                                                               Embryophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
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                                                                                                                                                                                                           Cinnamomum
                                                                                                                                                                                                                                                                                                                 precursor
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504

501

441

384

381

321 264 278 206

324

Tracheophyta;

protein)

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RESULT 4
Q94BW5
ID Q94B
AC Q9AB
AC QAC QAC
AC QC
D 0948W5
D 0948W5
LC 0948W5;
CC 0948W5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Type 2 ribosome-inactivating protein cinnamomin I prec (EC 3.2.22) (rRNA N-glycosidase).

CE (EC 3.2.2 (TRNA N-glycosidase).
                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                Qy
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Best Local Similarity
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SMART; SM00458; RICIN; 2.
PROSITE; PS50231; RICIN, B_LECTIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
Pfam; PF00552; Ricin_B_lectin; 6.
Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                             565
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 306;
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LYPLHGDPNQIWLPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DRCLTSTDNHSQGSIIIISSCSPGSEGQRWVFMNDGTILNLKNGLVMDVKGSNPSLHQII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNCLTS-DSNIRETVVKILSCGPASSGQRWMFKNDGTILNLYSGLVLDVRASDPSLKQII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RQGWLAGNNTEPFVTSIVGFNDLCMQANGDAMWVVECESSKAEQKWALYPDGSIRPHQDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOGWLPTNNTQPFVTTIVGLYGLCLQANSGQVWIEDCSSEKAEQQWALYADGSIRPQQNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYI 219
                                                                                                                                                                                                                                                                                                                                                                                          IWPATGKPNQQWLPL 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GYSAGDYVMIYDCRTPVTAASIWQFWANGTIINPQSALVLSAESGNPRTTLTVQANIYAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GYSPGVYVMIYDCNTAATDATRWQIWDNGTIINPRSSLVLAATSGNSGTTLTVQTNIYAV 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPIVRIVGRNGLCVDVRDGRFHNGNAIQLWPCKSNTDANQLWTLKRDNTIRSNGKCLTTY 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VGSVSDRVISGLAIMLFICRSSDRTSSDQFIDHLLMIRPILVDVADVATDADNDDTCADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVSI---LIPIIALMVYRCAP---PPSSQF---SLLIRPVVPNF-----NADVCMDP 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EYRVRESITRAEMFRPDPAMLSLENKWSALSNAVQQSNQGGVFSSPVEL--RSISNKPVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLERVAGELREEILLGMDPLENAISAL--WTSNLNQQRALARSLIVVIQMVAEAVRFRFI 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YPIINETTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPTVRISGRNGLCVDVRDGKYNNGNPIQLWPCKQNSDVNQLWTLRRDGTIRSNGKCLTTN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AADSPVALAVDVTNAYVVAYRTGSQSFFLREDNPD--PAIENLLPDTK-RYTFPFSGSYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        580 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64265 MW;
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55.1%;
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TYPE 2 RIBOSOME-INACTIVATING PROTEIN CINNAMOMIN II.

; 37E4289ECCE0CBFF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1487; DB 10; Pred. No. 6.7e-113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 141;
                                                                                                                            precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 580;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      564
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -I- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

EMBL; AY039801; AAK82458.1; -.

InterPro; IPR00072; Ricin_B_lectin.

InterPro; IPR001574; RIP.

Pfam; PF00652; Ricin_B_lectin; 5.

Pfam; PF00161; RIP, 1.

PRINTS; PR00396; SHIGARICIN.

SMART; SM00458; RICIN, 2.

PROSITE; PS50231; RICIN_B_LECTIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JUN-2001) to the EMBL/GenBank/DDBJ-1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yang Q., Gong Z.Z., Liu W.Y.;
"Molecular cloning of three type 2 RIP
genes encoding cinnamomin proteins and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; Signal; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             patterns.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=13429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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   565
                             560 ILYPLHGDPNQIWLPL 575
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                                                                                                                                                                                                                       382
                                                                                                                                                                                                                                                     325
                                                                                                                                                                                                                                                                                                           265 VGSVSDRVISGLAIMLFICRSTDRASSDQFIDHMLMIRPILVDVAEVATDADNDDTCADP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                299;
                                                                         D--NCLTSDSNIRETVVKILSCGPASSGORWMFKNDGTILNLYSGLVLDVRASDDSLKQI
                                                                                                                                       SQGWLPTUNTQPFYTTIVGLYGLCLQANSGQVWIEDCSSEKAEQQWALYADGSIRPQQNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
IIWPATGKPNHEWLPL
                                                          GPAACPLLDNHPQGSIIIISSCSPGSEGRRWVFMNDGTVLNLKNGLVMDVKGSNPSLHQI
                                                                                                                                                                                   GYSAGDYVMIYDCRTPVTAASIWQFWANGTIINPQSALVLSAESGNPRTTLTVQANIYAS
                                                                                                                                                                                                         GYSPGVYVMIYDCNTAATDATRWQIWDNGTIINPRSSLVLAATSGNSGTTLTVQTNIYAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                      RLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSN-
                                                                                                                       RQGWLAGNNTEPFVTSIVGFNDLCMQANGDAMWVEECESSKAEQKWALYPDGSIRPHQDP
                                                                                                                                                                                                                                                                    EPIVRIVGRNGLCVDVRDGRFHNGNAIQLWPCKSNTDANQLWTLKRDNTIRSNGKCLTTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AADSPVTLAVDVTNAYVVAYRTGSQSFFLREDNPD--PAIENLLPDTK-RYTFPFSGSYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYD
                                                                                                                                                                                                                                              EPTYRISGRNGLCVDVRDGKYNNGNPIQLWPCKQNSDVNQLWTLRRDGAIRSNGKCLTTN
                                                                                                                                                                                                                                                                                                                                          DVSI---LIPITALMVYRCAP---PPSSQF---SLLIRPVVPNF-----NADVCMDP
                                                                                                                                                                                                                                                                                                                                                                         EYRVRGSISRAEMFRPDPAMLSLENKWSALSNAVQQSNQGGVFSSPVEL--RSISNKPVY
                                                                                                                                                                                                                                                                                                                                                                                                        EGEMRTRIRYNRRSAPDPSVITLENSWGRLSTAIQESNQ-GAFASPIQLQRRNGSKFSVY
                                                                                                                                                                                                                                                                                                                                                                                                                                      DLEGVAGERREEILLGMDPLENAISALWISNL--NQQRALARSLIVVIQMVAEAVRFRFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YQTVTFTTKNATKTSYTQFIEALRAQLASGEE-PHGIPVMRERSTVPDSKRFILVELSNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           581 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64215 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 2.4e-109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE 2 RIBOSOME-INACTIVATING PROTEIN
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study of their expression
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N-GLYCOSIDIC
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RESULT

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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00396; SHIGAI SMART; SM00458; RICIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00652; Ricin_B_lectin;
Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cinnamomum camphora (Camphor tree)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-glycosidase) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NON_TER
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  473 GPAACPLLDNHPQGSIIIISSCSPGSEGRRWVFMNDGTVLNLKNGLVMDVKGSNPSLHQI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYI 219
                                                                                                                                                                                                                                   GYSPGYYYMIYDCNTAATDATRWQIWDNGTIINPRSSLVLAATSGNSGTTLTVQTNIYAV 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AADSPYTLAVDYTNAYVVAYRTGSQSFFLREDNPD--PAIENLLPDTK-RYTFPFSGSYT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAELSYTLALDYTNAYVYGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYD 159
                           D--NCLTSDSNIRETVVKILSCGPASSGQRWMFKNDGTILNLYSGLVLDVRASDPSLKQI
                                                                                                                                   SQGWLPTNNTQPFVTTIVGLYGLCLQANSGQVWIEDCSSEKAEQQWALYADGSIRPQQNR
                                                                                                                                                                                                          GYSAGDYVMIYDCRTPVTAASIWQFWANGTIINPQSALVLSAESGNPRTTLTVQANIYAS
                                                                                                                                                                                                                                                                                                                                                                                                                     \tt VGSVSDRVISGLAIMLFICRSTDRASSDQFIDHMLMIRPILVDVAEVATDADNDDTCADP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DVSI---LIPIIALMVYRCAP---PPSSQF---SLLIRPVVPNF-----NADVCMDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DLEGVAGERREEILLGMDPLENAISALWISNL--NQQRALARSLIVVIQMVAEAVRFRFI 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YQTVTFTTKKATKTSYTQFIEALRAQLASGEE-PHGIPVMRERSTVPDSKRFILVELSNW 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSN-
                                                                                                     {\tt RQGWLAGNNTEPFVTSIVGFNDLCMQANGDAMWVEECESSKAEQKWALYPDGSIRPHQDP}
                                                                                                                                                                                                                                                                                                                EPTVRISGRNGLCVDVRDGKYNNGNPIQLWPCKQNSDVNQLWTLRRDGAIRSNGKCLTIN
                                                                                                                                                                                                                                                                                                                                                              EPIVRIVGRNGLCVDVRDGRFHNGNAIQLWPCKSNTDANQLWTLKRDNTIRSNGKCLTTY 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EYRVRGSISRAEMFRPDPAMLSLENKWSALSNAVQQSNQGGVFSSPVEL--RSISNKPVY 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EGEMRTRIRYNRRSAPDPSVITLENSWGRLSTAIQESNQ-GAFASPIQLQRRNGSKFSVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   549 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60648 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.2%; Score 1441.5; DB 10; Length 53.8%; Pred. No. 3.3e-109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ricinus communis (Castor bean).

Ricinus communis (Castor bean).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids_I; Magpighiales; Euphorbiaceae; Ricinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q41143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 communis agglutinin gene from the castor plant Ricinus plant Mol. Biol. 9:287-295(1987). EMBL; M17631; AAA63506.1; -. HSSP; P02879; 2AAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RICIN E BETA CHAIN.
              Q06076;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Abrin-d (EC 3.2.2.22) (rRNA N-glycosidase) (Fragment).
Abrus precatorius (Indian licorice) (Crab's eye).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ladin B.F., Murray E.E., Halling A.C., Halling K.C., Tilakarathe N., Long G.L., Houston L.L., Weaver R.F.; "Characterization of a cDNA encoding ricin E, a hybrid ricin-Ricinus".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50231; RICIN_B_LECTIN; PROSITE; PS00338; SOMATOTROPIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001400; Somatotropin.
Pfam; PF00652; Ricin_B_lectin; 6.
SMART; SM00458; RICIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3988;
                                                                                                        Q06076
 Eukaryota; Viridiplantae;
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                                                                                                                                                                                  241
                                                                                                                                                                                                                                                                                                                                                              61 GKCLTTYGYSPGVYVMIYDCNTAATDATRWQIWDNGTIINPRSSLVLAATSGNSGTTLTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246;
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                                                                                                                                                                                                                                                            IRPQQNRDNCLTSDSNIRETVVKILSCGPASSGQRWMFKNDGTILNLYSGLVLDVRASDP
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                                                                                                                                                                                                                                                                                                                                                                                                                                        ADVCMDPEPIVRIVGRNGLCVDVRDGRFHNGNAIQLWPCKSNTDANQLWTLKRDNTIRSN
                                                                                                                                                                                                                                                                                                                                                                                            GKCLTTYGYSPGVYVMIYDCNTAATDATRWQIWDNGTIINPRSSLVLAATSGNSGTTLTV
                                                                                                                                                                                                                                                                                                                                                                                                                          ADVCMDPEPIVRIVGRNGLCVDVRDGRFHNGNAIQLWPCKSNTDANQLWTLKRDNTIRSN
                                                                                                                                                                                  SSLKQIIVHPFHGNLNQIWLPLF
                                                                                                                                                                                                              -SLKQIILYPLHGDPNQIWLPLF 576
                                                                                                                                                                                                                                                                                                     QTN1YAVSQGWLPTNNTQPFVTT1VGLYGMCLQANSGKVWLEDCTSEKAEQQWALYADGS
                                                                                                                                                                                                                                              IRPQQNRDNCLTTDANIKGTVVKILSCGPVSSGQRWMFKNDGTILNLYNGLVLDVRRSDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               263 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RICIN_B_LECTIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29134 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44.0%;
93.5%;
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 Streptophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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   Embryophyta; Tracheophyta;
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           Q8RXH6;
                         Q8RXH6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50231; RICIN_B_LECTIN; PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00396; SHIGARICIN. SMART; SM00458; RICIN; 2.
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J. MOL. Biol. 229:263-267(1993).
-i- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-93132798; PubMed-8421313;
Hung C.-H., Lee M.-C., Lee T.-C., Lin J.-Y.;
"Primary structure of three distinct isoabrins determined by cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIFIC ADENOSINE ON THE 28S RRNA
                                                                                                                                                                                 410
                                                                                                                                                                                                                                                                                         398
                                                                                                                                                                                                                                                                                                                           290
                                                                                                                                                                                                                                                                                                                                                                                               232
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 DLERWAHQTREEISLGLQALTHAIS---FLRSGASNDEEKARTLIVIIQMASEAARYRCI 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 RLEQLAGNLRENIELGNOPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYI 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 HAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYD 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            59 SERESIEVGIDVTNAYVVAYRAGSQSYFL---RDAPASASTYLFPGTQ-RYSLRFDGSYG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40 QYPIINFTTAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINORFILVELSN 99
                                                                                                                    ILSCGPASSGORWMFKNDGTILNLYSGLVLDVRASDPSLKQIILYPLHGDPNQIWLPLF 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                       VAEATYWEIWDNGTIINPKSALVLSAESSSMGGTLTVQTNEYLMRQGWRTGNNTSPFVTS 409
                                                                                                  LMACSNGWASQRWLFKNDGSIYSLYDDMVMDVKGSDPSLKQIILWPYTGKPNQIWLTLF 528
                                                                                                                                                                    ISGYSDLCMQAQGSNVWLADCDNNKKEQQWALYTDGSIRSVQNTNNCLTSKDHKQGSPIV 469
                                                                                                                                                                                                      IVGLYGLCLQANSGQVWIEDCSSEKAEQQWALYADGSIRPQQNRDNCLTSDSNIRETVVK 517
                                                                                                                                                                                                                                                            ATDATRWQIWDNGTIINPRSSLVLAATSGNSGTTLTVQTNIYAVSQGWLPTNNTQPEVTT 457
                                                                                                                                                                                                                                                                                                                                                                                                                  VS-ILIPIIALMYYRCAPPPSSQFSLLIRPVVPNFNADVCMDP-EPIVRIVGRNGLCVDV 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SNRVGVSIRTGTAFQPDPAMLSLENNWDNLSGGVQQSVQDAFPNNVILSSINRQPVVVDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EGEMRTRIRYNRRSAPDPSVITLENSWGRLSTAIQESNQGAFASPIQLQRRNGSKFSVYD
                                                                                                                                                                                                                                                                                                              YDDGYHNGNRIIAWKCKDRLEENQLWTLKSDLTIRSNGKCLTTEGYAPGNYVMIYDCTSA
                                                                                                                                                                                                                                                                                                                                  RDGREHNGNAIQLWPCKSNTDANQLWTLKRDNTIRSNGKCLTTYGYSPGVYVMIYDCNTA 397
                                                                                                                                                                                                                                                                                                                                                                                LSHPTVAVLALMLFVCNPPNANQSPLLIRSIVE -- ESKICSSRYEPTVRIGGRDGMCVDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QDQVIKFTTEGATSQSYKQFIEALRQRLTGG--LIHDIPVLPDPTTVEERNRYITVELSN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     528 AA;
                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43.2%; Score 1317.5; DB 10; Length 528; 50.3%; Pred. No. 4.3e-99; ative 77; Mismatches 178; Indels 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58870 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62ED42FB8FFE60F8 CRC64;
                    531 AA.
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InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50231; RICIN_B_LECTIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00652; Ricin_B_lectin; 6. Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Lectin chain A isoform 1 (EC 3.2.2.22) (rRNA N-glycosidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Viscum album (Indian) mRNA for Mistletoe lectin chain A isoform 1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Paramasivam M., Misra V., Srinivasan A., Singh T.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Spermatophyta; Magnoliophyta; eudicotyledons; Santalales; Viscaceae; Viscum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Viscum album (European mistletoe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                521 CGPASSGQRWMFKNDGTILNLYSGLVLDVRASDPSLKQIILYPLHGDPNQJWLPL 575
                                                                                                  461 LYGLCLQANSGOVWIEDCSSEKAEQQWALYADGSIRPQQNRDNCLTSDSNIRETVVKILS 520
                                                                                                                                                                      401 ATRWOIWDNGTIINPRSSLVLAATSGNSGTTLTVQTNIYAVSQGWLPTNNTQPFVTTIVG
                                                                                                                                                                                                          296 DFHDGNQIQLWPSKSNNDPNQLWTIKRDGTIRSNGSCLTTYGYTAGVYVMIFDCNTAVRE
                                                                                                                                                                                                                          341 REHNGNAIQLWPCKSNTDANQLWTLKRDNTIRSNGKCLTTYGYSPGVYVNIYDCNTAATD
                                                                                                                                                                                                                                                                              239 SLAIMLFYCGERPSSSDYRYWPLYIRPYIAD --- DVTCSASEPTYRIYGRNGMCYDYRDD
                                                                                                                                                                                                                                                                                                                286 IIALMVYRCAPPPSSQ----FSLLIRPVVPNFNADV-CMDPEPIVRIVGRNGLCVDVRDG
                                                                                                                                                                                                                                                                                                                                                                                  226 RIRYNRRSAPDPSVITLENSWGRLSTAIQESNQGAFASPIQLQRRNGSKFSVYDVSILIP 285
                                                                                                                                                                                                                                                                                                                                                                                                                       123 GH-RDQIPLGIDQLIQSVTALRF---PGGNTRTQARSILILIQMISEAARFNPILWRARQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           106 TLALDVINAYVYGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48 TAGATYQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPIN--QRFILVELSNHAELSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SM00458; RICIN; 2.
CSAGSSGQRWVFTNEGAILNLKNGLAMDVKGSNPKLRQIIIYPATGKPNQMWLPV 530
                                                                    FRDLCMESNGGSVWVETCVSSQQNQRWALYGDGSIRPKQNQDQCLTCGRDSVSTVINIVS
                                                                                                                                     AT IWQIWGNGTIINPRSNLALAASSGIKGTTLTVQTLDYTLGQGWLAGNDTAPREVTIYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAAIDYTNLYVVAYQAGDQSYFLR-DAPRGAE--THLFTGT-TRSSLPFNGSYPDLERYA 122
                                                                                                                                                                                                                                                                                                                                                 YINSGASFLPDVYMLELETSWGQQSTQVQQSTEGVFNNPIRLAIPPGNFVTLTNVRDVIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82; Mismatches
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LECTIN B CHAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Cloning of Viscum album subsp. coloratum (Korean mistletoe).";
Biochem. Biophys. Res. Commun. 0:0-0(2002).
-i- CAMALYTIC ACTIVITY: ENDOMPROLIXSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.
-i- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL; AF369961; BAL40017.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Santalales; Viscaceae; Viscum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
VCA precursor (EC 3.2.2.2) (rRNA N-glycosidase).
Viscum album subsp. coloratum.
Viscum album subsp. coloratum.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8W243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00396; SHIGARICIN.
SMART; SM00458; RICIN; 2.
PROSITE; PS50231; RICIN_B_LECTIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00652; Ricin_B_lectin; 6.
Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Park W.-B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=159976;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hydrolase; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POCST
                                                                                                                                                                                                                                                     237 TQVQQSTDGVFNNPFRLGISTGNFVTLSNVRDVIASLAIMLFVCRDRPSSSDVRYWPLVI
                                                                                                                                                                                                                                                                                     251 TAIQESNQGAFASPIQLQRRNGSKFSYYDVSILIPTIALMYYRCAPPPSSQ----FSLLI 306
                                                                                                                                                                                                                                                                                                                                                          191 TGGTQLPTLARSFIICIQMISEAARFQYIEGEMRTRIRYNRRSAPDPSVITLENSWGRLS 250
                                                                                                                                                                                                                                                                                                                                                                                                                             131 DNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPLEEAISALYYYS 190
     484
                                                                    424 TSGNSGTTLTVQTNIYAVSQGWLPTNNTQPFVTTIVGLYGLCLQANSGQVWIEDCSSEKA 483
                                                                                                                                           364 TLKRDNTIRSNGKCLTTYGYSPGYYYMIYDCNTAATDATRWQIWDNGTIINPRSSLVLAA 423
                                                                                                                                                                                                                    307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          280;
                                                                                                           353 TIRRDGTIGSNGRCLTTYGYTAGVYVVIFDCNTAVREATLWQIWGNGTIINPRSNLVLGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15 VATWLCFGSTSGWSFTLEDNNIFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVR 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 VSCFLMLGLVFGATVKAETKFRYERLRLRVTHQTTG---DEYFRFTTLLRDYVSSGS-FS 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                  RPVVPNFNA--DV-CMDPEPIVRIVGRNGLCVDVRDGRFHNGNAIQLWPCKSNTDANQLW 363
                                                                                                                                                                                                                                                                                                                                                                                             DGAE----RHLFTGT-TRSSLPFTGSYTDLERYAGH-RDQIPLGIEELIQSVSAL-RYS 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HEIPVLPNRVGLPIN--QRFILVELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFH--P 130
                                                                                                                                                                                                                                                                                                                          GGSTR--AQARSLIILIQMISEAARFNPIFWRARQYINSGESFLPDMYMLELETSWGQQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NEIPLL-ROSTIPVSDAQRFVLVELTNQGGDSITAAIDVTNLYVVAYQAGDQSYFLRDAP 126
 EQQWALYADGSIRPQQNRDNCLTSDSNIRETVVKILSCGPASSGQRWMFKNDGTILNLYS
                                                                                                                                                                                RPVLENSGAVDDVTCTASEPTVRIVGRDGLCVDVRDGKFYNGNPIQLWP-----WDPNQLW
                                     ASGSSGTTLTVQTQVYFLGQGWLAGNDTAPREVTIYGFGNLCMEANGASVSVETCGGSKE 472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               565 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             273
565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62401 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            42.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VCA ALPHA CHAIN.
VCA BETA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               991E3994DA005F11 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               565 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; DB 10;
1.8e-96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 565;
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                                                                                                                                                                                          352
                                                                                                                                                                                                                                                                                                                                   236
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RESULT 10
Q9M6E9
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Primary Structure and Function Analysis of the Abrus precatorius Aggluthnin A Chain by Site-directed Mutagenesis: Pro199 of Amphiphilic alpha-Helix H Impairs Protein Synthesis Inhibitory Activity.";

J. Biol. Chem. 275:1897-1901(2000).

- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 285 RRNA.

SPECIFIC ADENOSINE ON THE 285 RRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Preproagglutinin (EC 3.2.2.22) (TRNA N-glycosidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9M6E9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9M6E9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=20102702; PubMed=10636890;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liu C.L., Tsai C.C., Lin S.C., Wang L.I., Hsu C.I., Hwang M.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Abrus precatorius (Indian licorice) (Crab's eye)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pfam; pF00652; Ricin_B_lectin; 6.
pfam; pF00161; RIP; 1.
pRINTS; pR00396; SHIGARICIN.
SMARR; SM00458; RICIN; 2.
pROSITE; pS50231; RICIN_B_LECTIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P11140; 1ABR.
InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50231; RICIN_B_LECT: PROSITE; PS00275; SHIGA_RICIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF190173; AAF28309.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 40.8%; Score 1244; DB 10; Length 547; Local Similarity 47.4%; Pred. No. 4.6e-93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     544 GLYLDVRASDPSLKQIILYPLHGDPNQIWLPL 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               533 GLVMDVAQSNPSLRRIIIYPATGKPNQMWLPV 564
                                                                                                                                                                                                                                            148 NRYTFAFGGNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICI 207
               322 EPIVRIVGRNGLCVDVRDGRFHNGNAIQLWPCKSNTDANQLWTLKRDNTIRSNGKCLTTY 381
                                                     239 INVRQERVVVSSLSHPSVSAL----ALMLFVCNPLNATQSPLLIRSVVE--QSKICSSHY 292
                                                                                                                                                                                                          123 -QYSLPFDGNYDDLEKWAHQSRQRISLG----LEALRQĞIKFLRSGASDDEEIARTLIVII 178
                                                                                                                                                                                                                                                                                                                                                                                                 31 LEDNNIFPKQY-PIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVL--PNRVGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                           263;
                                                                                                                                                                                                                                                                                      68 --NQYVTVELSYSDTVSIQLGIDLTNAYVVAYRAGSESFFF---RNAPASASTYLFTGTQ
                                                                                                                                                                                                                                                                                                                        88 INQREILVELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQ 147
                                                                                                                                                                                                                                                                                                                                                              10 LHGNAYYQAQFQDPIKFTTGSATPASYNQFIDALRERLTGG--LIYGIPVLRDPSTVEKP
                                                                                           ----ORRNGSKFSVYDVSILIPITALMVYRCAPPPSSQFSLLIRPVVPNFNADVCMDP- 321
                                                                                                                                 QMVAEAARFRYVSKLVVISLSNRAAFQPDPSMLSLENTWEPLSRAVQHTVQDTFPQNVTL 238
                                                                                                                                                                       QMISEAARFQYIEGEMRTRIRYNRRSAPDPSVITLENSWGRLSTAIQESNQGAFASPIQL 267
Toxin. 547 AA; 61248 MW; 355A325C2354A1BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Pred. No. 4.6e-93; 87; Mismatches 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
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   Indels 26; Gaps
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                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Van Damme E.J.M., Peumans W.J.;

"Iris (Iris hollandica var. Professor Blaauw) plants express both type
1 and type 2 ribosome-inactivating proteins in bulb tissue.";

Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 28S RRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00396; SHIGARICIN.
SMART: SM00458; RICIN, 2.
PROSITE; PS50231, RICIN_B_LECTIN; 2.
PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Iris hollandica (Dutch iris).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Iridaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00652; Ricin_B_lectin; Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -I- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=35876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-glycosidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or-mak-2003 (TERMHITE). 23, Last annotation update)
Ribosome-inactivating protein IRAb (EC 3.2.2.2) (rRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8W2E7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8W2E7
174 LGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIBGEMRTRIRYN----
                                                                  124 QAQGHYYLLHDTPDNPQLYGSDA------HRLSFDGSYPALQHVAGEYRENID
                                                                                                                                                                                                                                                                 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      442
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                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                     TTGADVRHEIPVLPNRVGLPI------NQRFILVELSNHAELSVTLALDVTNAYVVGY 119
                                                                                                             RAGNSAYFFH--PDNQE----DAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIE
                                                                                                                                                          SSGT-----SEYGIPLMRAQNPSSSQELLLVEIFGWDNEPVTLVLNLVNAYVIAY 123
                                                                                                                                                                                                                                                  IWIWWAAIVGPAILVCSSSLSVTRGGHKNLP--YKKVEFHITGCTKDTYSAFIQSLRTHL
                                                                                                                                                                                                                                                                                           IVIWMYAVATWLCFGSTSGWSFTLEDNNIFPKQYPIINFTTAGATVQSYTNFIRAVRGRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GYSPGYYYMIYDCNTAATDATRWQIWDNGTIINPRSSLYLAATSGNSGTTLTYQTNIYAV 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RQGWRTGNDTSPFVTSIAGFFKLCMEAHGNSMWLDVCDITKEEQQWAVYPDGSIRPVQNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GYAPGNYVMIYDCSSAVAEATYWDIWDNGTIINPKSGLVLSAESSSMGGTLTVQKNDYRM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPYTGNANQMWATLF 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YPLHGDPNQIWLPLF 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NNCLTCEEHKQGATIVMMGCSNAWASQRWVFKSDGTIYNLYDDMVMDVKSSDPSLKQIIL 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SQGWLPTNNTQPFVTTIVGLYGLCLQANSGQVWIEDCSSEKAEQQWALYADGSIRPQQNR 501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EPTVRIGGRDGLCVDVSDNAYNNGNPIILMKCKDQLEVNQLWTLKSDKTIRSKGKCLTTY 352
                                                                                                                                                                                                                                                                                                                                                                                                                                          592 AA; 65677 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Toxin.
                                                                                                                                                                                                                                                                                                                                                    Conservative 101;
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                                                                                                                                                                                                                                                                                                                                                                       36.3%;
                                                                                                                                                                                                                                                                                                                                             Pred. No. 5.7e
                                                                                                                                                                                                                                                                                                                                                         Score 1109; DB 10
No. 5.7e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                   6F1F335ECF8A99E3 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                        DB 10;
                                                                                                                                                                                                                                                                                                                                               196;
                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                        Length 592;
                                                                                                                                                                                                                                                                                                                                             70;
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                                                                                                                                   ACCOCCE RTT RN RN DDR DDR DDR RT RN RN DDR DDR DDR RT RN DDR DDR RT RN DDR R
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RESULT 12
                                                                                  Query Match
Best Local
                                                              Matches
                                                                                                                                                           SEQUENCE
                                                                                                                                                                                  Hydrolase; Toxin.
NON_TER 1
                                                                                                                                                                                                                      PROSITE; PS50231; RICIN_B_LECTIN; PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                                                                          PRINTS; PR00396; SHIGARICIN. SMART; SM00458; RICIN; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Van Damme E.J.M., Peumans W.J.;

"Iris (Iris hollandica var. Professor Blaauw) plants express both type
1 and type 2 ribosome-inactivating proteins in bulb tissue.";

Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
-i- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 28S RRNA.
                                                                                                                                                                                                                                                                                                                         Pfam; PF00652; Ricin_B_lectin;
Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                       -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING EMBL; AF256084; AAL55093.1; -INTERPROPORTS: RIP. Bectin. InterPro; IPR0001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Ribosome-inactivating protein IRAr (EC 3.2.2.22) (IRNA N-glycosidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2002 (TrEMBLrel. 20, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Iris hollandica (Dutch iris).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=35876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8W2E8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8W2E8
                                                           230;
41 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPI-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               585 NOMWETTE 592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171 LGINELGSAILVLHQWSP-PTVERTVARSFIVLIQMVSEAARFRAIE----TRVRRNIIQ
                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THDQGSQIILLSCNFGGASQRWMFTSQGTIYNLHSGYVMDVKQSDPSLQQIIIWSTTGNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SNIRETVVKILSCGPASSGQRWMFKNDGTILNLYSGLVLDVRASDPSLKQIILYPLHGDP 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NTQPFVTTIVGLYGLCLQANSGQ-VWIEDCSSEKAEQQWALYADGSIRPQQNRDNCLTSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MIYDCNTAATDATRWQIWDNGTIINPRSSLVLAATSGNSGTTLTVQTNIYAVSQGWLPTN 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MIYDCSSAVMGATLWTMY-NGSLINRPSGLAISAESGESGTTLTMQVHLNASKQGWLPSN 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNGLCYDVRDGRFHNGNAIQLWPCKSNTDANQLWTLKRDNTIRSNGKCLTTYGYSPGVYV 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NQIWLPLF 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NTRPFLTPIIGINGLCVQRNDQEDVGLATCDDNNSNQKWYLYGDGSIRPLTDPNYCVTSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RDGYCMDVKDGLYHNGNPVTLSSCKQNNDVNQFWTFKSDGTIQSNGKCLTAYGYNAGAYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -- IALMVYRCAPPPSSQFSL-------LIRPVVPNFNADVCMDPEPIVRIVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VGDYRSFRPGAGMLDLETNWGTLSERVQESNEGVFANRLTLQTTNFETIHIYNAQTARQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----RRSAPDPSVITLENSWGRLSTAIQESNQGAFASPIQLQRRNGSKFSVYDVSILIPI 286
                                                                                                                                                      573 AA;
                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Magnoliophyta; Liliopsida; Asparagales;
                                                                                                                                                        63759 MW;
                                                                             35.4%;
                                                      101;
                                              Score 1081; DB 10;
Pred. No. 1.1e-79;
)1; Mismatches 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                1414A3B9AECD4F5C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   573 AA.
                                                                                               Length 573;
                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Iridaceae;
                                                   68;
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       584
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--- NQRF 92

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RESULT 13
Q9AVR2
Q9AVR
Q9AVR
AC Q9AVR
DT 01-JU
DT 01-M
DT 01-M
DE Ribo
DE N-91
GN EBU1
GN FR G1:
GN G1:
GN
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                          HSSP; P02879; 2AAI.
InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
InterPro; IPR001574; RIP.
Pfam; PF00652; Ricin_B_lectin; 6.
Pfam; PF00161; RIF; 1.
PRINTS; PR00396; SHIGARICIN.
SMART; SM00458; RICIN; 2.
                                                                                                                                                                                  Q9Avr2;
Q9Avr2;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Ribosome-inactivating protein precursor (EC 3.2.2.22) (TRNA
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=28503;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Spermatophyta; Magnoliophyta; eudicotyledons; core eudic
Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sambucus ebulus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-glycosidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9AVR2
                                                                                                                                                                                                                                                                                                                                                 TISSUE=Leaf;
    PROSITE; PS50231; RICIN_B_LECTIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YDKVEFHITGCTKDTYSAFIQSLRTHLSSGT-----SEYGIPLMRAQNPSSSQQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YSGLVLDVRASDPSLKQIILYPLHGDPNQIWLPLF 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NSNQKWYLYGDGSIRPLIDPTYCVTSQTHDQGSQIILLSCNFGGASQRWMFTSQGTIHNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LNVVRSMLDIVEDDTCPLSEPTMRISGRDGYCMDVKDGLYHNGNPVTLSSCKQNNDVNQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --LIRPVVPNFNADVCMDPEPIVRIVGRNGLCVDVRDGRFHNGNAIQLWPCKSNTDANQL 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IQMVSEVARFRAIE----TRVRRNIIQVGDYRSFRPGAGMLDLETNWEPLSERVQESNEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSGYVMDVKQSDPSLQQIIIWSTTGNPNQMWFTTF 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KAEQQWALYADGSIRPQQNRDNCLTSDSNIRETVVKILSCGPASSGQRWMFKNDGTILNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                      PROTEIN FAMILY
                                                                                                                                                                                                                                                                   AT ONE
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RESULT
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Best Local
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Glycosidase; Hydrolase; Signal; Toxin
SIGNAL 1 25 POTENTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tr. Spermatophyta; Magnoliophyta; eudicotyledons; core eudi-
Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus
                                                                                                                                                                                                                                                     01-JUL-1997 (TrEMBLrel. 01-OCT-2002 (TrEMBLrel.
   derived from a truncated
                                                  MEDLINE=98112023; PubMed=9450339; Van Damme E.J., Roy S., Barre A.,
                                                                                                                                                                                                    Sambucus nigra (European elder).
                                                                                                                                                                                                                   N-glycosidase).
                                                                                                                                                                                                                                    Ribosome inactivating protein precursor
                                                                                                                                                                                                                                                                                          01-JUL-1997
                                                                                                                                                                                                                                                                                                           004367;
                                                                                                                                                                                                                                                                                                                              004367
"The major elderberry (Sambucus nigra) fruit protein is a lectin derived from a truncated type 2 ribosome-inactivating protein.";
                                                                                          SEQUENCE FROM N.A.
                                   Peumans W.J.
                                                                                                                              NCBI_TaxID=4202;
                                                                                                                                                                                                                                                                                                                                                              14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YPSYSFNLAGAKSTTYRDFLKNLRDRVATGTYEVNGLPYLRRESEVQVKNRFVLVRLTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNLETAAGTRRESIELGPNPLDGAITSLWY--DGG-----VARSLLVLIQMVPEAARFRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMITDCSTAAEDATKWEVLIDGSIINPSSGLVMTAPSGASRTTLLLENNIHAASQGWTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VMIYDCNTAATDATRWQIWDNGTIINPRSSLVILAATSGNSGTTLTVQTNIYAVSQGWLPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRDGLCVDVRNGYDTDGTPIQLWPC--GTQRNQQWTFYNDKTIRSMGKCMTANGLNSGSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GRNGLCVDVRDGRFHNGNAIQLWPCKSNTDANQLWTLKRDNTIRSNGKCLTTYGYSPGVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I EQEVRRSLOQLTSFTPNALMLSMENNWSSMSLEVQLSGDNVSPFSGTVQLQNYDHTPRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IEGEMRTRIRYNRRSAPDPSVITLENSWGRLSTAIQES--NQGAFASPIQLQRRNGSKFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NGDTVTSAVDVTNLYLVAFSANGNSYFF-----KDATELQKSNLFLGT-TQHTLSFTGNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NNTQPFVTTIVGLYGLCLQAN--SGQVWIEDCSSEKAEQQWALYADGSIRPQQNRDNCLT
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                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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41.6%;
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04, Last sequence update)
. 22, Last annotation update)
. 7- recursor (EC 3.2.2.22) (rRNA
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                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                          Rouge P.,
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                                                                                                                                                                    core eudicots;
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Best Local S
Matches 234
QBSA43;
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, 2.2.22) (TRNA N-91ycosidase
                                                                                          Q8SA43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00652; Ricin_B_lectin; Pfam; PF00161; RIP; 1.
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InterPro; IPR001574; RIP.
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CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.
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                                                                                                                                                                                                                                   WIEDCSSEKAEQQWALYADGSIRPQQNRDNCLTSDSNIRETVVKILSCGPASSGQRWMFK
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                                                                                                                                                            SNGAIVNPNSTLVMDVKANDVSLREIIIFPSHGDPNQQWV
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                                                                                                                                                                                                                                                                                              RSSLVLAATSGNSGTTLTVQTNIYAVSQGWLPTNNTQPFVTTIVGLYGLCLQAN--SGQV
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                                                                                                                                                                                                                    WMENCEVTSLQQQWALFGDRTIRVNSDRGLCVTTNGYHSKDLIIILKCQGLPS-QRWFFN
                                                                                                                                                                                                                                                                                                                                                            NTDANQLWTLKRDNTIRSNGKCLTTYGYSPGVYVMIYDCNTAATDATRWQIWDNGTIINP
                                                                                                                                                                                                                                                                                                                                                                                          {\tt SAIRRPHVLAGEDNKYNDGETCPIPASFTRRIVGRDGLCVDVRDGYDTDGTPIQLWPCGS}
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSMSLEVQQSGDNVSPFTGTVQLQNYDHTPRLVDNFEELYKITGIAILLFRCFSP--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YYDE-----SVARSLLVVIQMVSEAARFRYIEQEVRRSLQQTAGFTPNALMLSMENNW
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563 AA;
                                                                                         PRELIMINARY;
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297 R
563 R
62336 MW;
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RIBOSOME INACTIVATING PROTEIN,
RIBOSOME INACTIVATING PROTEIN,
RIBOSOME INACTIVATING PROTEIN,
3ED286C08E796205 CRC64;
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               N-glycosidase)
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                                                                                                                                                                                                                                                                                                                                                            В
                                                                                                                                                                                                                                                                                                                                                                                       QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SQ PTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COOK J.P., Roberts L.M., Lord M.;

New Isoform of Abrin - Abrin G.";

Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT O

SPECIFIC ADENOSINE ON THE 28S RRNA.

-!- SIMILARITY: BELDONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

EMBL; AF479636; AAL77434.1; -.

InterPro; IPR001772; Ricin_B_lectin.

InterPro; IPR001574; RIP.

Pfam; PF00652; Ricin_B_lectin; 6.

Pfam; PF00652; Ricin_B_lectin; 6.

Pfam; PF00161; RIP; 1.

CMARE. SMOALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00161; RIP; 1.

SMART; SM00458; RICIN; 2.

PROSITE; PS0231; RICIN B_LECTIN; PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Abrus precatorius (Indian licorice) (Crab's eye).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hydrolase; Toxin.
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                          304
                                                                                       498
                                                                                                                    244
                                                                                                                                                                              184
                                                                                                                                                                                                                                        124
364
                                                                                                                                                                                                                                                                                                                                                                          200 ARSFIICIQMISEAARFQYIEGEMRTRIRYNRRSAPDPSVITLENSWGRLSTAIQESNQG
                                                                                                                                                                                                                                                                                                                              260 AFASPIQLQRRNGSKFSVYDVS-ILIPIIALMVYRCAPPPSSQFSLLIRPVVPNFNADVC
                                                                                                                                                                                                                                                                                                                                                                                                                        197;
                                                                                                                                                                                                                                                                                                    99
                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                            QIILYPLHGDPNQIWLPLF
                                                                        QQNRDNCLTSDSNIRETVVKILSCGPASSGQRWMFKNDGTILNLYSGLVLDVRASDPSLK
                                                                                                                  DYRMRQGWRTGNDTSPFVTSIAGYSDLCMEAHESNMWLADCDRNKKEQQWALYPDGSIRP
                                                                                                                                                                           LTTYGYSPGVYVMIYDCNTAATDATRWQIWDNGTIINPRSSLVLAATSGNSGTTLTVQTN
|||||| || |||||| :| :|| :|||||||||:|:||| | | |||| |
LTTYGYDPGNYVMIYDCTSAVPEATYWEIWDNGTIINPKSALVLSAESSAMGGKLTVQKN
                                                                                                                                                                                                                                                      MDP-EPIVRIVGRNGLCVDVRDGRFHNGNAIQLWPCKSNTDANQLWTLKRDNTIRSNGKC
                                                                                                                                                                                                                                                                                                  TFPNDVTLRNIRDEPVIVNSLSHPTVAVLALMLFVCNPPNANQSPLLIRSIVE--KSDTC
                                                                                                                                                                                                                                      VPPTEPTVRIGGRDGMCVDVSDEAYNNGNPIILWKCKDQLEEKQLWTLKSDKTIRSKGKC
                                                                                                                                                                                                                                                                                                                                                           ARTLIVIIOMVAEAARFRYISNRVGASIRTGTAFQPDPAMISLENNWGRLSGGVQQATQD
QIILWPYTGKPNQIWLTLF
                                                          VQNTNNCLTSKDHKQGSTIVLMGCSNGWASQRWVFKNDGSVYSLYDDMVMDVKGSDPSLK
                                                                                                                                              IYAVSQGWLPTNNTQPFVTTIVGLYGLCLQANSGQVWIEDCSSEKAEQQWALYADGSIRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116
382
                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1
>105
>382
382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42743 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                    34.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1053;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABRIN
ABRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B08AB341813AD2EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₿ Þ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 10;
..1e-77;
                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BOND AT ONE
                                                                                                                                                                                                                                                                                                                                                                                                                     4;
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                  303
                                                                                                                                              497
                                                                                                                                                                            243
                                                                                                                                                                                                         437
                                                                                                                                                                                                                                                                   377
                                                                                                                                                                                                                                                                                                123
                                                                                                                                                                                                                                                                                                                             318
                                                                                                                                                                                                                                                                                                                                                            65
                                                                                                                                                                                                                                      183
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completed: September 16,
me : 95.8773 secs

2003,

11:49:13

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Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perfect score:
                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                              Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq length: 0 seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A_Geneseq_19Jun03:*
1: /SIDS1/gcgdata/gei
2: /SIDS1/gcgdata/gei
3: /SIDS1/gcgdata/gei
  100.0
100.0
100.0
100.0
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                                                                                                                                                                                                                              Query
Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-083-336A-2
948
1 MKPGGNTIVIWMYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          September 16, 2003, 11:29:47; Search time 29.8072 Seconds (without alignments) 953.195 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1107863 seqs, 158726573 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                          SIDSI/gcgdata/geneseq/geneseqp-embl/AA1980.DAT: *
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1981.DAT: *
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1982.DAT: *
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1983.DAT: *
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1983.DAT: *
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1983.DAT: *
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1986.DAT: *
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1987.DAT: *
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1989.DAT: *
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1990.DAT: *
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1991.DAT: *
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1991.DAT: *
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1991.DAT: *
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1991.DAT: *
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1992.DAT: *
SIDSI/gcgdata/geneseq/geneseqp-embl/AA1993.DAT: *
SIDSI/gcgdata/geneseq/geneseqp-embl/AA2000.DAT: *
SIDSI/gcgdata/geneseq/geneseqp-embl/AA2001.DAT: *
SIDSI/gcgdata/geneseq/geneseqp-embl/AA2001.DAT: *
SIDSI/gcgdata/geneseq/geneseqp-embl/AA2001.DAT: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MKPGGNTIVIWMYAVATWLC......RLEQLAGNLRENIELGNGPL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd
332
332
332
576
576
576
576
  18
20
21
22
                                                                                            10
8
                     AAP70838
) AAP95639
) AAP90079
AAP70326
3 AAW25787
) AAW55892
AAY78592
                                                                                                                                                                                 AAP70097
                                                                                                                                                                                                                              H
                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1107863
                                        Sequence of Ricinu
Castorbean ricin.
Castor bean ricin
                                                                                                        Sequence of Ricinu
Ricin A encoded by
Ricin D. Ricinus
                                                                                                                                                                               Ricin A. Escheric
                                                                                                                                                                                                                            Description
                     Ricinus communis r
```

## ALIGNMENTS

RESULT 1 AAP70097

AAP70097 standard; protein; 332 AA

Ricin A; Met-aminopeptidase

Escherichia coli.

Ricin A. 09-APR-1991 AAP70097;

(first entry)

```
Castor bean prepro
 N-terminal methionine free proteins prodn. - by using host transformed with vector to express a methionine-amino-peptidase
                     WPI; 1987-110172/16.
N-PSDB; AAN70152.
                                                                        06-MAY-1986;
20-SEP-1985;
                                           Benbassat A, Bauer KA,
                                                                                              19-SEP-1986;
                                                                                                             22-APR-1987.
                                                                                                                            EP219237-A.
                                                         (CETU ) CETUS CORP.
                                                                       86US-0860330.
85US-0778414.
                                                                                              86EP-0307242
                                           Chang S,
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Chang SY;

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RESULT 2
AAP70838
ID AAP7
XX
  Qy
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                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                                                      В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            SXCCXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
The full-length sequences encoding ricin A (AAN70520), ricin
             Disclosure; Fig 1; 112pp; English.
                                                                                                              07-MAR-1986;
                                                                                                                          13-NOV-1986;
                                                                                                                                                                         Region
                                                                                                                                                                                                           Key
                                                                                                                                                                                                                                                                             25-MAR-2003
18-FEB-1991
                                                                                                                                                                                                                                                                                                  AAP70838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         using Met-aminopeptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ricin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig. 4; 20pp; English.
                                  New non-glycosylated ricin precursor and toxin etc.
by recombinant DNA procedures with specific isolation
                                                                            Piatak M;
                                                                                                                                        23-SEP-1987
                                                                                                                                                                                      Region
                                                                                                                                                                                                   Region
                                                                                                                                                                                                                        Ricinus communis
                                                                                                                                                                                                                                     plant toxin.
                                                                                                                                                                                                                                                               Sequence of Ricinus communis castor beans ricin toxin (RT
                                                                                                                                                                                                                                                                                                               AAP70838 standard;
                                                                                         (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                            Lectin; toxin protein; cytotoxic; cytostatic; castor bean
                                                                                                                                                                                                                                                        protein encoded by pRA123.
                                                             1987-265177/38
                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                              121
                                                                                               ) CETUS CORP
                                                                                                                                                                                                                                                                                                                                                                          A may be produced in a f
Met-aminopeptidase from
                                                       AAN70519.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                        AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPL 179
                                                                                                                                                                                                                                                                                                                                                                                                      AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPL 179
                                                                                                                                                                                                                                                                                                                                                                                                                   MKPGGNTIVIWMYAVATWLCFGSTSGWSFTLEDNNIFPKQYPIINFTTAGATVQSYTNFI
                            soluble prods
                                                                                                                                                                                                                                                                                                                                                                                                                                                            332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                             (updated)
(first entry)
                                                                                                             86US-0837583.
                                                                                                                           86EP-0308877
                                                                                                                                                                        /note="A-chain"
315..332
                                                                                                                                                                   /note="B-chain"
                                                                                                                                                                                       /note="Leader"
33..302
                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                               protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a form which lacks an N-terminal Met
rom E.coli.
                                                                                                                                                                                                                                                                                                               332
                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 948; DB 8;
Pred. No. 1.6e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                               A
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                  are prepd
steps for
                                                                                                                                                                                                                                                                or ricin)
                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                      60
                                                                                                                                                                                                                                                                                                                                                                                                                   60
                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
  맑
                                                                                                                                                                                                                                                                                                 Qy
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                                                                                                                                                                                                                                                                                                                          Qy
                                                                                                                                                                                                                                                                                                                                         Вb
                                                                                                                                                                                                                                                                                                                                                      Qγ
                                                                                                                                                                                                                                                                                                                                                                                                88888888888888888888888
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RESULT 3
AAP95639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AAN70525), putative ricin E (AAN70526) and RCA (AAN70524) in precursor form were obtd. using messenger RNA to obtain a cDNA library, and then probing the library to retrieve the desired cDNA inserts. The clibrary was probed using the 35-mer given in AAN70514. Figure 4 (see AAN70520, AAN70521, AAN70522) shows the nucleotide sequences of three classified contg. cDNA inserts obtd. by probing a cDNA library for sequences encoding ricin B using the probe in AAN70517. The cDNA inserts can be placed into expression vectors. Site-directed mutagenesis may be used to place an ATG start codon and a HindIII coling sequences of the inserts can be ligated into expression vectors. The coding sequences of the inserts can be ligated into expression vectors contg. the PhoA promoter-operator and leader sequence (QAAN7053) and suitable retrooregulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                     08-FEB-1984;
08-FEB-1984;
09-FEB-1984;
07-SEP-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                               04-OCT-1989
                                                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ricinus communis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ricin A encoded by insert from plasmid pRA123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-2003
31-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAP95639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAP95639 standard; protein; 332
                                                                                                                                     19-JAN-1989;
                                                                                                                                                                                                                           EP335476-A.
                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid pRA123; ricin-A; ricin-B; cytotoxicity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 AGNSAYFFHPDNQEDAFAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MKPGGNTIVIWMYAVATWLCFGSTSGWSFTLEDNNIFPKQYPIINFTTAGATVQSYTNFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MKPGGNTIVIWMYAVATWLCFGSTSGWSFTLEDNNIFPKQYPIINFTTAGATVQSYTNFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (updated)
(updated)
(first entry)
84US-0578121.
84US-0578122.
84US-0648759.
84US-0653515.
                                                                                        84US-0578115
                                                                                                                                     89EP-0201162
                                                                                                                                                                                                                                                                                                                                                                                   /label= leader sequence 36..302
                                                                                                                                                                                                                                                                                             /label=linker
315..332
                                                                                                                                                                                                                                                                                                                                         303..314
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                        /label=B-chain
                                                                                                                                                                                                                                                                                                                                                            /label=A-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 948; DB 8;
Pred. No. 1.6e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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0;

Gaps

60 60

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RESULT 4
AAP9007
ID AAP9
XX AAP9007
XX AAP9
XX AAP9
XX AAP9
XX AAP9
XX Picl
DE Ricl
DE Ricl
DE Ricl
XX Ricl
XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gelfand D, Piatak MJ;
                                                                                                                                                                                                                                                                                                                       Ricin D; Ricinus modified; lectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Updated
(Updated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid RA123 (ATCC No. 39799) carries the entire coding sequence for ricin A, as well as codons for 12 AAs joining the A to the B chain. Following modification for ease of manipulation the plasmid was used construct expression vectors which express the conjugates in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 14; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombinant vectors expressing ricin chains or diphtheria toxin -used for prodn. of new immunotoxin conjugates with monoclonal antibodies, having high cell specificity and good extracellular stability.
     WPI; 1989-178366/24.
N-PSDB; AAN90068.
                                                          Brown EL,
                                                                                                                                                                                                                                                                                                                                                                              Ricin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAP90079
                                                                                             (GEMY ) GENETICS INST INC
                                                                                                                                24-NOV-1987;
                                                                                                                                                                     23-NOV-1988;
                                                                                                                                                                                                            01-JUN-1989
                                                                                                                                                                                                                                               W08904839-A
                                                                                                                                                                                                                                                                                  Ricinus communis
                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP90079 standard; protein; 562 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Updated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CETU ) CETUS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1989-286959/40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MKPGGNTIVIWMYAVATWLCFGSTSGWSFTLEDNNIFPKQYPIINFTTAGATVQSYTNFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MKPGGNTIVIWMYAVATWLCFGSTSGWSFTLEDNNIFPKQYPIINFTTAGATVQSYTNFI
                                                          Jones S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               n 31-OCT-2002
n 25-MAR-2003
n 25-MAR-2003
n 25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lawyer FC,
                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                  87US-0124735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                                     88WO-US04238
                                                                                                                                                                                                                                                                                                                     communis;
binding re
                                                                                                                                                                                                                                                                                  (caster beans).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8888
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                                                                                                                                                                                                                                                                                                                       ;; caster beans; Zanibariensis variety;
removed; reduced cell binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               add missing OS field.)
correct PF field.)
correct PR field.)
correct PI field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 948; DB 10;
Pred. No. 1.6e-92;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Greenfield L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nitecki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     . 332;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified ricin molecules and toxin conjugates - in which the lectin binding function of the B is removed or diminished to reduce cell binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to toxins to eliminate cell binding (Updated on 25-MAR-2003 to correct P (Updated on 25-MAR-2003 to correct P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ricin D (see corresp. AAN90068) found on the EcoRI-HindIII fragment of DNA from Ricinu communis, Zanibariensis variety. Patent discloses many modifications of ricin in which the lectin binding function of the B chain is diminished or removed, and conjugation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; fig 1;
                                      Piatak M;
                                                                                                                                                                                                                                                                                                                                                                            Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence of R. (RT or ricin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAR-2003
21-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAP70326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAP70326 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                        (CETU ) CETUS CORP
(CHIR ) CHIRON COR
                                                                                                                                07-MAR-1986;
                                                                                                                                                                     13-NOV-1986;
                                                                                                                                                                                                          23-SEP-1987
                                                                                                                                                                                                                                           EP237676-A.
                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                                                                                  Ricinus communis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plant toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lectin; toxin protein;
   1987-265177/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MKPGGNTIVIWMYAVATWLCFGSTSGWSFTLEDNNIFPKQYPIINFTTAGATVQSYTNFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            562 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ricinus communis (castor bean)
n) E precursor encoded by pRT38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (updated)
(first en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                              86US-0837583
                                                                                                                                                                     86EP-0308877
                                                                                                                                                                                                                                                                                                                                   /note= "leader"
36..302
                                                                                                                                                                                                                                                                                                  /note= "A-chain"
315..576
                                                                                                                                                                                                                                                                                  /note= "B-chain'
                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytotoxic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   correct PA field.)
correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 948; DB 10;
Pred. No. 3.1e-92;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ą
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytostatic; castor bean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ricin toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 562;
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뭐 Qy В QΥ В Qy

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RESULT 6
AAW25787
ID AAW2
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AC AAW2
XX
AC AAW2
XX
AC CAS
AC C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The full length sequences encoding ricin A (AAN70520), ricin D CC (AAN70525) putative ricin E (AAN70526) and RCA (AAN70524) in precursor CC form were obtained, using the messenger RNA to obtain a cDNA library, and CC library was probed using the messenger RNA to obtain a cDNA library, and CC (Library was probed using the 35-mer given in AAN70514. Figure 4 (see CC AAN70520, AAN70521, AAN70522), shows the nucleotide sequences of three CC plasmids containing cDNA inserts obtained by probing a cDNA library CC for sequences encoding ricin B using the probe in AAN70517. The cDNA CC inserts can be placed into expression vectors. Site-directed containing the mature protein, (see AAN70518). The CC coding sequences of the inserts can be ligated into expression coden and a Hindill CC site at the beginning of the mature protein, (see AAN70518). The CC coding sequences of the inserts can be ligated into expression cC (AAN70523) and suitable retroregulators.

CC (AAN70523) and suitable retroregulators.

CC (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
      16-SEP-1997.
                                                                      US5668255-A
                                                                                                                                                                   Domain
                                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ricinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cell binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Castorbean ricin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW25787 standard; Protein; 576 AA.
                                                                                                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cell binding ligand; translocation domain; diphtheria to: interleukin-2; T-cell lymphoma; organ rejection; therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-MAR-2003
27-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW25787
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New non-glycosylated ricin precursor and toxin etc. - are prepd
by recombinant DNA procedures with specific isolation steps for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; AAN70526
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 100.0%;
Local Similarity 100.0%;
les 179; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytotoxin; hybrid protein; cell delivery;
inding ligand; translocation domain; diphtheria toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     communis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      576 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (updated)
(first entry)
                                                                                                                                                                   /label
                                                                                                                                                                                                                                                                                           /label= Sig_peptide 36..302
                                                                                                                                     /label= B-domain
                                                                                                                                                                                                                                                             /label= A-domain
                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                              - Linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 948; DB 8;
Pred. No. 3.2e-92;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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RESULT 7
AAY55892
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This polypeptide comprises the castorbean cytotoxin, ricin.

CD DNA (see AAT91638) encoding the enzymatic A domain and a portion CC DNA (see AAT91638) encoding the enzymatic A domain and a portion CC DIA (see AAT91638) encoding the enzymatic A domain and a portion CC DIA (see AAT91638) encoding the enzymatic A domain and a portion CC cricin-diphtheria toxin B'-interleukin-2 gene that was expressed in CC E. coli. The hybrid protein can be isolated and used to treat CC conditions involving over-production of cells bearing IL2 receptors, such as certain T-cell lymphomas and organ transplant rejection CC crises. The hybrid inactivates ribosomes in cells bearing IL2 receptors, resulting in cessation of protein synthesis and death of CC target cells. Claimed hybrid proteins comprise a translocation CC domain and a cell binding domain from e.g. a hormone, growth factor CC or polypeptide toxin. The hybrid molecules can be used for the CC labels) into cells. The use of a translocation mechanism ensures that the hybrid will be effective in relatively low doses, since a that the hybrid will be effective in relatively low doses, since a contractive of the contractive of the target will be taken into the contractive of the target will be taken into the contractive of the taken into the contractive of the target will be taken into the contractive of the target will be taken into the contractive of the target will be taken into the contractive of the target will be taken into the contractive of the target will be taken into the contractive of the target will be taken into the contractive of the target will be taken into the contractive of the target will be taken into the contractive of the target will be taken into the contractive of the target will be taken into the contractive of the target will be taken into the contractive of the target will be taken into the contractive of the target will be taken into the contractive of the target will be target will be target will be target will be target of the target will be target 
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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07-JUN-1984;
25-APR-1985;
07-JUN-1985;
07-JUN-1989;
22-DEC-1989;
14-JUN-1990;
04-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               high proportion of the substance of interest will be taken into the targeted cells. The hybrid molecules can be manufactured as a single hybrid recombinant protein, permitting reproducibility, consistency, and the precise control of composition. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New hybrid molecules for delivery of agents to cells - comprise a binding domain of a cell binding ligand and a portion of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-470103/43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-AUG-1993;
                           AAY55892;
                                                                              AAY55892 standard; Protein; 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 4; Fig 11A-B; 30pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  translocation domain of a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Murphy JR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SERA-) SERAGEN
                                                                                                                                                                                                                                             121 AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPL 179
                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                                     61 RAVRGRLITTGADVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MKPGGNTIVIWMYAVATWLCFGSTSGWSFTLEDNNIFPKQYPIINFTTAGATVQSYTNFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKPGGNTIVIWMYAVATWLCFGSTSGWSFTLEDNNIFPKQYPIINFTTAGATVQSYTNFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                           RAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYR 120
                                                                                                                                                                                                                 AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  576 AA;
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85US-0726808.
85US-0742554.
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93US-0102387.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 948; DB 18; 100.0%; Pred. No. 3.2e-92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Castor bean ricin toxin

15-FEB-2000 (first entry)

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CC protein comprising three parts: (a) the first part conding a nybrid of the binding domain of a cell-binding polypeptide ligand allowing the hybrid protein to bind to an animal cell; (b) the second part comprises chybrid protein to bind to an animal cell; (b) the second part comprises comprises of a bortion of a translocation domain of a naturally occurring protein comprises. It toxin, both the covin, both linum neurotoxin, ricin, cholera covin, LT toxin, C3 toxin, shiga-like toxin, pertussis toxin and tetanus covin, which translocate the third part of the across the cytoplasmic committee into the cytosol of the cell; and (c) the third part comprises covin, which translocate the third part of the across the cytoplasmic covin, which is non-native coving protein of (b). This sequence represents the castor bean ricin toxin sequence for use in generating the hybrid of the castor bean ricin toxin sequence for use in generating the hybrid of the castor bean ricin toxin sequence for use in generating the hybrid of the castor bean ricin toxin sequence for use in generating the hybrid of the castor bean ricin toxin sequence for use in generating the hybrid of the castor bean ricin toxin sequence for use in generating the hybrid of the castor the disease. The hybrid is especially used in treating calleviate or cure the disease, by delivering to affected cells an enzyme complying the missing function, to supplementing cellular levels of a particular enzyme or a scarce precursor or cofactor, to directing toxins concert colline toxins to destroy particular cells (such as adipocytes, cancer coll, or virus infected-cells), to counteracting viral infections such as concert in the process of getting non-therapeutic substances such as detectable labels into cells.
                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant DNA molecule encoding a three part hybrid protein used the treatment of Aids and genetic deficiency diseases - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translocation domain; botulinum; neurotoxin; ricin; cholera; tetanus; shiga-like toxin; pertussis; translocation; cytoplasmic membrane; HIV cytosol; therapy; genetic deficiency disease; enzyme; co-factor; pois
                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; Fig 11; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Murphy
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22-DEC-1989;
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07-JUN-1984;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         adipocyte; cancer; virus; infection; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-APR-1985
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                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention relates to a recombinant DNA molecule encoding
                                                                                                                                                                                                                                                                                                Similarity
RAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYR 120
                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          A,
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89US-0456095.
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91US-0722484.
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                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                  Score 948; DB 20;
Pred. No. 3.2e-92;
; Mismatches 0;
                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                      Length 576;
                                                                                                                                                                                                                                                      0;
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Ş В Qy

RAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYR

introducing into appropriate cells antibodies to

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RESULT 8
AAY78592
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      the third part across the cytoplasmic membrane and into the cytosol of the cell. The third part comprises a chemical entity to be introduced into the cell, where each of the first and third part is non-native with respect to naturally occurring protein, and the covalent bond attaching the second and third part is cleavable. The toxin represented by the present sequence can form part of the third portion of the hybrid protein. The cell binding domain binds to a specific cell and the translocation domain transfers the hybrid molecule across the cell membrane into the cytosol. The third part of the protein, linked to the translocation domain through a cleavable bond, can then carry out its function. The hybrid molecules are useful for treating genetic deficiency diseases by delivering to affected cells an enzyme supplying the missing function, to supplement cellular levels of a particular enzyme or a scarce precursor or cofactor, to direct toxins or other poisons to virus-infected cells), and to counteract viral infections such as HIV by introducing into annorminate cells antibodies to virus-infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-1984;
27-JUN-1991;
25-APR-1985;
07-JUN-1985;
                                                                                                                                                                                                                                                                                                                             This sequence represents the Ricinus communis ricin protein sequence. The toxin can be included in the hybrid protein of the invention and used to destroy or modify the cell that the hybrid protein is targeted to. The hybrid protein comprises a first part which is a portion of the binding domain of a cell-binding ligand, effective to cause the hybrid molecule to bind to a cell of an animal. The second part comprises a portion of a translocation domain of anaturally occurring protein (e.g. the translocation domain of diphtheria toxin) the second part translocates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New two-part hybrid protein comprising a translocation domain and cell-binding domain, for treating genetic deficiency diseases, can and HIV infections - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ricin; toxin; hybrid protein; translocation domain; cell destruction; cell binding domain; genetic deficiency disease; cell targetting; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; Fig 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-AUG-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-FEB-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   adipocyte; enzyme delivery; anti-viral; HIV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ricinus communis ricin protein sequence
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85US-0742554.
85US-0456095.
89US-0436095.
90US-0538276.
93US-0102387.
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91US-0722484.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
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RRESULT 9
AAG78301
IID AAG78
XX AAG7
XX AAG7
XX Cast
XX Cast
XX Cast
XX Price
XX Pri
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           CCCCXXX PTT TT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
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The sequence relates to preproricin protein encoded by the DNA sequence given in AAI64138. The invention relates to a novel toxin (e.g., ricin) based antiviral agent which is toxic to virus-infected cells, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Castor bean plant; preproricin; ricin; A chain; B chain; human immunodeficiency virus infection; HIV; toxin; antiviral agent; retroviral infection; anti-HIV; virucide activity; viral protease.
                                                                                                                                                                                              Novel composition comprising toxin e.g., useful for treating viral infections such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Castor bean
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAG78301 standard; Protein; 576
                                                                                                                Disclosure; Page 50-54; 66pp; English.
                                                                                                                                                                          virus infection.
                                                                                                                                                                                                                                                                                     N-PSDB; AAI64138.
                                                                                                                                                                                                                                                                                                               WPI; 2001-581908/65
                                                                                                                                                                                                                                                                                                                                                                     Keener WK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-FEB-2000; 2000US-0182759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-FEB-2001; 2001WO-US05282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ricinus communis.
                                                                                                                                                                                                                                                                                                                                                                                                                         (BECH-) BECHTEL BWXT IDAHO LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 RAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYR 120
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                                                                                                                                                                                                                                                                                                                                                                     Ward TE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Linker_|
/note= "Cleaved 315..576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "N-glycosidase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= Ricin_A_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= Signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Galactose/N-acetylgalactosamine-binding lectin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ricin_B_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Linker_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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Pred. No. 3.2e-92;
); Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          activation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2).
                                                                                                                                                                                                    ricin based antiviral compound has human immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of ricin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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Keener WK,

Ward TE

(BECH-) BECHTEL BWXT IDAHO LLC 16-FEB-2000; 2000US-0182759 15-FEB-2001; 2001WO-US05282

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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 179; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     non-toxic to uninfected cells. The invention has anti-HIV and virucide activities. Its mechanism of action is through inactivation of cellular ribosomes and enhancement of binding of the antiviral agent to galactose residues on cell surfaces, and its cellular internalisation. The invention is useful for treating human immunodeficiency virus infection and other viral infections, especially retroviral infections. The antiviral agent is activated in viral particles or early-stage infected cells, killing the cells upon infection and effectively preventing the integration of the viral genome into the host genome thereby preventing the latency/rebound problem. The agent enters all HIV susceptible cells, and not just cells known to act as host cells for the virus. The antiviral agent remains inert in a cell until degraded in it, unless the cell is infected with the virus, where the viral protease activates it.
                                                                                                                                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                                                                                                                                      Castor bean plant; preproricin; ricin; A chain; B chain; human immunodeficiency virus infection; HIV; toxin; antiviral agent; retroviral infection; anti-HIV; virucide activity; viral protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG78302 standard; Protein; 576 AA
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                                                                                                                                                       WO200160393-A1
                                                                                                                                                                                                                   Protein
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                                                                                                                                                                                                                                                                                                                Protein
                                                                                                                                                                                                                                                                                                                                                                                           Ricinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Castor bean preproricin protein (SEQ ID 3).
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                                                                                                                                                                                                                                                                                                                                           Peptide
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                                                                                                                                                                                                                                                                                                              /label= Signal peptide 36..302
                                                                                                                                                                                                                                                                  303..314
                                                                                                                                                                                                                                  /label= Linker_peptide
/note= "Cleaved during
                                                                                                                                                                                                                                                                               /label= Ricin_A_chain
/note= "N-glycosidase"
                                                                                                                                                                                                      /Label=
                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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                                                                                                                                                                                    "Galactose/N-acetylgalactosamine-binding
                                                                                                                                                                                                    Ricin_B_chain
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Pred. No. 3.2e-92;
); Mismatches 0;
                                                                                                                                                                                                                                     activation of ricin"
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RESULT 11
AAP70325
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AC AAP70
AC AAP70
XX 25-M2
DT 18-FE
XX Seque
DE Seque
DE D pre
XX Lecti
XW Plant
XX Plant
XX Ricir
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FT Regic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cc given in AAI64139. The invention relates to a novel toxin (e.g., ricin) cc based antiviral agent which is toxic to virus-infected cells, but cc non-toxic to uninfected cells. The invention has anti-HIV and virucide activities. Its mechanism of action is through inactivation of cellular ribosomes and enhancement of binding of the antiviral agent to galactose residues on cell surfaces, and its cellular internalisation. The cc invention is useful for treating human immunodeficiency virus infection cand other viral infections, especially retroviral infections. The cc and other viral infections, especially retroviral infections. The cc antiviral agent is activated in viral particles or early-stage infected cc ells, killing the cells upon infection and effectively preventing the integration of the viral genome into the host genome thereby preventing the latency/rebound problem. The agent enters all HIV susceptible cells, cand not just cells known to act as host cells for the virus. The cc antiviral agent remains inert in a cell until degraded in it, unless the cc cell is infected with the virus, where the viral protease activates it.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 54-57; 66pp; English.
                                                                   Region
                                                                                                     Region
                                                                                                                                         Region
                                                                                                                                                                                                Ricinus
                                                                                                                                                                                                                                  plant toxin.
                                                                                                                                                                                                                                                   Lectin; toxin
                                                                                                                                                                                                                                                                                     D precursor
                                                                                                                                                                                                                                                                                                       Sequence of
                                                                                                                                                                                                                                                                                                                                           18-FEB-1991
                                                                                                                                                                                                                                                                                                                                                              25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP70325 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel composition comprising toxin e.g., ricin based antiviral compound useful for treating viral infections such as human immunodeficiency
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 RAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYR 120
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                                                                                                                                                                                                                                                                                                         Ricinus
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                                                                                                                                                                                                                                                                                                                                         (updated)
(first entry)
                                                                                                                                                                                                                                                 protein;
                                                                   /note="A-chain"
313..574
                                                                                                                                                        Location/Qualifiers
                                                                                                                        /note="Leader"
                                                                                                                                                                                                                                                                                                                                                                                                                                  protein;
                                                                                                                                                                                                                                                                                     communis castor beans ricin toxin by pRT17.
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                                                                                                                                                                                                                                                   cytotoxic; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    574 AA
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Pred. No. 3.2e-92;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The full-length sequences encoding ricin A (AAN70520), ricin D (AAN70525), putative ricin E (AAN70526) and RCA (AAN70524) in precursor form were obtd. using messenger RNA to obtain a cDNA library, and then probing the library to retrieve the desired cDNA inserts. The library was probed using the 35-mer given in AAN70514. Figure 4 (see AAN70520, AAN70521, AAN70522) shows the nucleotide sequences of three plasmids contg. cDNA inserts obtd. by probing a cDNA library for sequences encoding ricin B using the probe in AAN70517. The cDNA inserts can be placed into expression vectors. Site-directed mutagenesis may be used to place an AFG start codon and a Hindill site at the beginning of the mature protein (see AAN70518). The coding sequences of the inserts can be ligated into expression vectors contg. the PhoA promoter-operator and leader sequence (AAN7053) and suitable retroregulators.

(Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
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                                                                                                                                          10-MAR-2003
04-JAN-1991
                                                                                                                                                                                       AAR06554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Piatak M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-MAR-1986;
                           US4948729-A
                                                      Ricinus communis
                                                                                  Alkaline phosphatase; phoA;
                                                                                                             Ricin A gene product of plasmid
                                                                                                                                                                                                                  AAR06554 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 13(1-2); 112pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        purer and soluble prods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New non-glycosylated ricin precursor and toxin etc. - are pr
by recombinant DNA procedures with specific isolation steps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAN70525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-NOV-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-SEP-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1987-265177/38
                                                                                                                                                                                                                                                                                                        123 NSAYFFHPDNOEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPL 179
                                                                                                                                                                                                                                                                                          121 NSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPL 177
                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                              63 VRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYRAG
                                                                                                                                                                                                                                                                                                                                                                                                            _
                                                                                                                                                                                                                                                                                                                                                                                                                         3 PGGNTIVIWMYAVATWLCFGSTSGWSFTLEDNNIFPKQYPIINFTTAGATVQSYTNFIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHIRON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                 PGGNT I V I I WAYAVAT WLC FGSTSGWSFTLED NNI FPKQYPI I NFTTAGAT VQSYTNFIRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             574 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                          (updated)
(first en
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86US-0837583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86EP-0308877
                                                                                                                                                                                                                  protein;
                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 938; DB 8;
Pred. No. 3.7e-91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                insert pRA123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       are prepd
steps for
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Вp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pho A leader sequence can be used to manufacture genes encoding soluble, active, heterologous proteins for a bacterial expression system. Heterologous ricin A is soluble in the sonicate of cells and may be readily purified without detergent.

(Updated on 10-MAR-2003 to add missing OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alkaline phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Soluble, biologically active protein prodn. in procaryotic using terminated leader DNA sequence encoding bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-MAR-1988;
25-MAR-1985;
24-JUL-1987;
                                                    20-JUL-1988;
                                                                                                         09-FEB-1989
                                                                                                                                                              W08901037-A
                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                 Baculovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ricin; toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA sequence of ricin toxin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-JUL-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAP94793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 8; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAQ05786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Piatak M, Laird WJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-MAR-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP94793 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CETU ) CETUS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1990-267900/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 RAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MKPGGNTIVIWMYAVATWLCFGSTSGWSFTLEDNNIFPKQYPIINFTTAGATVQSYTNFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MKPGGNTIVIWMYAVATWLCFGSTSGWSFTLEDNNIFPKQYPIINFTRAGATVQRYTNFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   baculovirus; muteins; ss
87US-0077126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88US-0171132.
85US-0715933.
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                                                    88WO-US02442
                                                                                                                                                                                                                   /label=B-chain
                                                                                                                                                                                                                                                                   /label=A-chain
                                                                                                                                                                                                                                                                                                                     /label=Leader peptide
                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lane JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 937; DB 11; Length 332; Pred. No. 2.3e-91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression
of cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hosts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
\begin{array}{c} \mathbf{I} \mathbf{D} \\ \mathbf{A} \\ \mathbf{C} \\ \mathbf{C}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           멍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  γ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW25136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                    09-DEC-1992;
11-JUN-1990;
26-JAN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Maize; proRIP; ribosome inactivating protein; alpha; beta subunit; internal linker; Barley Translation Inhibitor; Trichosanthin; Ricin A-chain; Abrin-A A-chain; Saporin; SLT-1; Luffin A; MAP; Ricinus communis agglutinin; Momordin; PAP-S; Luffin-B; Dianthin 30; therapeutic toxin; tumour cell targeted; protein synthesis inhibitor; post-translational modification; cancer; neoplasia; HIV: AIDS; human immunodeficiency virus; acquired immune deficiency syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant baculovirus transfer vectors - used for prodn. of ricin toxin in a baculovirus insect cell expression system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1989-061173/08.
N-PSDB; AAN91039.
Hey TD,
                                                                                                                                                                                                                                                                                                                                              US5646026-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW25136 standard; Protein; 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Recombinant baculovirus vector is capable of introducing ricin gene into virus genome, allowing creation of a insect cell/baculovirus ricin
                                                  (DOWC ) DOWELANCO.
                                                                                                                                                                                                                                         07-JUN-1995;
                                                                                                                                                                                                                                                                                              08-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ricin A-chain ribosome inhibitory protein inactive precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW25136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page -; 85pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-FEB-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CETU ) CETUS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 NSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 VRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYRAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NSAYFFHGDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPL 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Morgan AER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       574 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lane JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88US-0153778
                                                                                                       95US-0378761
95US-0485286
                                                                                                                                                         92US-0987927
90US-0535636
                                                                                                                                                                                                                                         95US-0485286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.0%;
Walsh TA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Piatak M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 929; DB 10;
Pred. No. 3.4e-90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clark R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 574;
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Gaps

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RESULT 15
AAW21699
ID AAW21
XX AW21
XX AW21
XX 25-M
DT 25-M
DT 26-SI
XX Pro-
KW inac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              eukaryotic ribosomes and hence preventing protein production. Many conditions and the produced with an internal linker including different RIPs may be produced with an internal linker including maize RIP, Trichosanthin, Ricin A-chain, Abrin-A A-chain and Saporin. The RIPs can be used in the construction of therapeutic toxins targeted to specific cells such as tumour cells via the can be used in the construction of the rapeutic toxins targeted to specific cells such as tumour cells via the can be used in HIV therapy (see Us4869903). There is interest in expressing RIP recombinantly in host eukaryotic cells, because of the capacity to provide correct post-translational processing. However, RIPs effectively inhibit protein synthesis in eukaryotic cells resulting in cell death. Since the inactive RIP proteins are not cytotoxic to cells converted to active RIP proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                             pro-Ribosome Inactivating Protein; proRIP; peptide linker; cancer;
inactivation; eukaryotic ribosome; alpha fragment; beta fragment;
inhibitor; protein synthesis; N-glycosidase; glycosidic bond; liver;
rat; ribosomal 28S RNA; cellular proliferation; HIV-infected T cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW25136 represents a Ricin A-chain ribosome inhibitory protein (RIP) which was engineered to contain a selectively removable internal peptide linker sequence separating the alpha and beta units of the RIP. When separated the two units regain activity and are capable of inactivating
                                       US5635384-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                             Region
                                                                                                                                                                  Ricinus communis.
                                                                                                                                                                                                                                                                                             Ricin A-chain RIP.
                                                                                                                                                                                                                                                                                                                                 25-MAR-2003
26-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                        AAW21699;
                                                                                                                                                                                                                                                                                                                                                                                                                         AAW21699 standard; Protein; 290 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Column 91-94; 186pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           precursors of ribosome inactivating proteins; eukaryotic cells without causing cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding pro-ribosome inactivating proteins - precursors of ribosome inactivating proteins; can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 NQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12 MYAVATWLCEGSTSGWSETLEDNNIFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72 DVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFFPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MYAVATWLCEGSTSGWSETLEDNNIFPKQYPIINETTAGATVQSYTNFIRAVRGRLTTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                290 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                           Location/Qualifiers 152..162
                                                                                            /note=
                                                                                                                                                                                                                                                                                                                              entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.4%;
                                                                      "Position of possible insertion peptide linker sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 885; DB 18;
; Pred. No. 6.8e-86;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              can be expressed
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                                                                                                                                                                                                                                                                                        The sequences given in AAW21698-710 represent Ribosome Inactivating CP Proteins (RIP's), which may be used in the construction of the protein of the invention. The proRIP has a selectively removable, internal peptide linker. The precursor sequence is incapable of inactivating eukaryotic ribosomes, but can be converted by removal of the linker into a protein having alpha and beta fragments and being capable of inactivating eukaryotic ribosomes. RIPs are potent inhibitors of eukaryotic protein synthesis. They possess a highly specific N-glycosidase activity which cleaves the glycosidic bond of adenine 4324 of rat liver ribosomal 28S RNA. RIP's selectively inhibit cellular proliferation of cells, e.g. cancer cells and HIV-infected T cellular proliferation of cells, e.g. cancer cells and HIV-infected T cells. The inactive proRIP proteins make it possible to provide protein consistive inhibitors with uses in practical and improved ways not before possible. The RIP can be used to make cytotoxic conjugates.
                                                                                                                                                                                                                                   Query Match
Best Local (
                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-DEC-1992;
11-JUN-1990;
26-JAN-1995;
                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inactive precursor of maize ribosome-inactivating protein - also chimeric ribosome-inactivating protein precursors containing internal linker sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
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121
                                 132 NQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPL
                                                                                                                                                                                                                    168;
                                                                     61 DVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPD
                                                                                      72 DVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFFPD
                                                                                                                                                              12 MYAVATWLCFGSTSGWSFTLEDNNIFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGA
                                                                                                                                           1 MYAVATWLCFGSTSGWSFTLEDNNIFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGA
                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOWELANCO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Column 91-94; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Morgan AER,
NQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPL
                                                                                                                                                                                                                                                                                          290
                                                                                                                                                                                                                 Conservative
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90US-0535636.
95US-0378761.
                                                                                                                                                                                                                                                                                        ΑĄ;
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                                                                                                                                                                                                                                93.4%;
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Pred. No. 6.8e-86;
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Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OM protein -
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               and is derived by a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed,
            Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Issued_Patents_AA:*
1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
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5: /cgn2_6/ptodata/1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-083-336A-2
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1 MKPGGNTIVIWMYAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         328717 seqs, 42310858 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gapop 10.0 , Gapext 0.5
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            GenCore version (c) 1993 - 2003
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US-07-988-430-1
US-08-425-336-1
US-08-488-113B-1
US-08-48-360-1
US-08-48-360-1
US-08-36-389-1
US-08-38-38-1
PCT-US-20-9487-1
US-08-356-786-8
US-08-38-7-31-1
US-08-488-113B-6
US-08-488-113B-6
US-08-488-113B-6
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US-08-488-113B-6
US-08-488-13B-6
US-08-488-13B-6
US-08-488-13B-6
US-08-488-13B-6
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Compugen Ltd.
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Sequence 27, Appli
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Sequence 17, Appli
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12 MYAVATWLCFGSTSGWSFTLEDNNIFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGA 71 MYAVATWLCFGSTSGWSFTLEDNNIFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGA 60

US-08-378-761A-27

STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein

protein

Query Match Best Local Similarity Matches 168;

93.4%; ilarity 100.0%; Conservative (

Length 290; Indels

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Gaps

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RESULT 1  US-08-378-761A-27  ¡ Sequence 27, Application US/08378761A  Patent No. 5635384  ¡ GENERAL INFORMATION:  APPLICANT: WALSH, TERENCE A  APPLICANT: HEY, TIMOTHY D  APPLICANT: HEY, TIMOTHY D  APPLICANT: HORGAN, ALICE ER  TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, IN  TITLE OF INVENTION: USING  NUMBER OF SEQUENCES: 81  CORRESPONDENCE ADDRESS:  ADDRESSEE: ANDREA T. BORUCKI  STREET: 9330 ZIONSVILLE ROAD  CITY: INDIANAPOLIS  STATE: IN  COUNTRY: US  STATE: IN  COUNTRY: US  COMPUTER READABLE FORM:  MEDIUM TYPE: Floppy disk  COMPUTER READABLE FORM:  MEDIUM TYPE: Ploppy disk  COMPUTER OF STATE: PATENTIN RELEASE #1.0, Version #1.25  SOFTWARE: PATENTIN RELEASE #1.0, Version #1.25  CURRENT APPLICATION NUMBER: US/08/378,761A  FILING DATE: 26-JAN-1995  CLASSIFICATION NUMBER: 3651  REFERENCE,DOCKET NUMBER: 3872B  TELEPHONE: (317) 337-44846  INFORMATION FOR SEQ ID NO: 27:  SEQUENCE CHARACTERISTICS:  LENGTH: 290 amino acids  TYPE: amino acids  TYPE: amino acids	ALIGNMENTS	28 265.5 28.0 267 1 US-08-485-286-74 29 265.5 28.0 289 1 US-08-184-237-4 30 265.5 28.0 289 2 US-08-184-237-4 31 265.5 28.0 289 2 US-08-482-920-4 32 265.5 28.0 289 3 US-08-483-502-4 33 265.5 28.0 289 3 US-08-283-301-15 36 265.5 28.0 289 4 US-09-726-651A-4 35 265.5 28.0 289 4 US-09-726-651A-4 36 265.5 28.0 289 1 US-08-378-761A-71 37 245 25.8 250 1 US-08-378-761A-71 37 245 25.8 250 1 US-08-38-873-3 39 240.5 25.4 290 1 US-09-58-873-3 39 240.5 25.4 290 2 US-08-245-754A-2 40 240.5 25.4 290 2 US-08-92-486-7 41 236.5 24.9 248 3 US-08-902-486-15 42 236.5 24.9 248 3 US-08-902-486-15 43 234 24.7 255 1 US-07-988-430-6 44 234 24.7 255 1 US-07-988-430-6
SS FOR MAKING A METHOD		Sequence 74, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 15, Appli Sequence 71, Appli Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 16, Appli Sequence 16, Appli

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Patent No. 5646026 5646119
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Best Local Similarity
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                                                                                                                                                                                                          Matches
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APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-
TITLE OF INVENTION: PRECURSOR
TITLE OF INVENTION: USING
NUMBER OF SEQUENCES: 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (317) 337-4846 INFORMATION FOR SEQ ID NO: 27
                                                                                                                                                                                                                                                                            MOLECULE TYPE:
-485-286-27
                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
NAME: BORUCKI, ANDREA T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/378761
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE:
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COMPUTER: IB
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STATE: IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 336
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
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121
                132 NQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPL 179
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                                                                                                  72 DVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPD 131
                                                                                                                                                                      12 MYAVATWLCFGSTSGWSFTLEDNNIFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGA 71
                                                                                                                                    I MYAVATWLCFGSTSGMSFTLEDNNIFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGA 60
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NQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPL 168
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9330 ZIONSVILLE ROAD
                                                                                                                                                                                                                                                                                                                                                             290 amino acids
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                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                            protein
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                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                      93.4%; score 885; DB 1; 1
100.0%; pred. No. 2.5e-94;
tive 0; Mismatches 0;
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RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TITLE OF INVENTION: DNA ENCODING INACTIVE PRECURSOR AND ACTIVE FORMS OF MAIZE RIBOSOME INACTIVATIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO:4:
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APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5376546and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27129/30910
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEPHONE: (312) 346-5750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 49
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: Materials Comprising and Methods of
TITLE OF INVENTION: Composition and Use for Ribosome-Inactivating Proteins
NUMBER OF SEQUENCES: 57
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                                                                                                                                                                                   CLASSIFICATION: 435 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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STREET: Street
CITY: Chicago
STATE: Illinois
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FILING DATE: 11-JUN-1990
                                                                                                                                                                                                                          APPLICATION NUMBER: UPFILING DATE: 19920619
                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Marshall ADDRESSEE: Bicknell
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                                                                                                                                                                                                                                                                                                                                                                                                                USA
                                                                                                                                                                                                                                                                                         SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.4%; Score 885; DB 6; Length 290; 100.0%; Pred. No. 2.5e-94; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                 us/07/901,707
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                                                                                                        APPLICATION NUMBER: US/07/988,430
FILING DATE: 19921209
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: NO. 5415202and, Greta E.
REGISTRATION NUMBER: 35302
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                INFORMATION FOR SEQ ID NO: 1:
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SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
                               REFERENCE/DOCKET NUMBER: 31133
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEPAX: (312) 984-9740
TELEX: 25-3856
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         USA
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Lei, Shau-Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Better, Marc D.
Carroll, Stephen F.
Lane, Julie A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bernhard, Susan L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Materials Comprising and Methods of Preparation and Use for Ribosome-Inactivating Proteins
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                                                                                                                                                                                                                       APPLICATION NUMBER: 08/064,691
FILING DATE: 12-MAY 1993
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                             TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acid
                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
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                                              TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                TOPOLOGY:
                                                                                                                                                                                             NAME: Meyers, Thomas REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 18-APF
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STATE: Illinoi
                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
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                                              H: 267 amino acids amino acid
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               protein
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N: 530
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ower, 233 South Wacker Drive
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Patent No.
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Best Local Similarity
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                                                                     TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 530
PRIOR APPLICATION DATA:
PRIOR NUMBER: US 08/425,336
                                                                                                       REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 08/00*,00-
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/988,430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                             FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNICHOLAS, Janet M.
                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 18-APR-PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
PRIOR APPLICATION DATA:
TYPE: ami
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COMPUTER: II
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                                                                                                                                                                                                                                                                                                                                            FILING DATE: 09-DEC-1992
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                                                                                                                                                                                  REGISTRATION NUMBER:
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                  amino acid
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                               267 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IBM PC compatible SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-JUN-1995
                                                                                                                                                                                                                                    UMBER: US 07/787,567
04-NOV-1991
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US-08-477-484B-1
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Best Local Similarity
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                              TELEX: 650 388-1248 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/988,430 FILING DATE: 09-DEC-1992 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 01 FILING DATE: 12-MAY-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,484B
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                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 18-APR-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
              SEQUENCE CHARACTERISTICS
                                                                                                   TELECOMMUNICATION INFORMATION:
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                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                                                 TELEFAX:
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                                                                                                                                                      McNicholas, Janet M
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500 West Madison Street, 34th floor
267 amino acids
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                                                                  : 312/707-8889
312/707-9155
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                                                                                                                                                                                                                                                             US 07/901,707
                                                                                                                                    32,918
                                                                                                                       11022US07/200-70.P3.C2A
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US-08-646-360-1
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 INFORMATION
                                                                                                                                                                                   APPLICATION NUMBER: US 08/
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 19-JUN-1992
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                             TELECOMMUNICATION INFORMATION: TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
                                                                                                                     APPLICATION NUMBER: US 0 FILING DATE: 04-NOV-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
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                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08 FILING DATE: 13-MAY-1996
                                                                           REFERENCE/DOCKET NUMBER:
                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER: II
                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2: McAndrews, Held & Malloy, Ltd.
500 West Madison Street, 34th floor
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                                                                                                                                                     US 07/787,567
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RESULT 10
US-08-839-765-1
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Best Local Similarity
ATTORNEY AGENT INFORMATION:

NAME: MCNICHOLAS, Janet M.

REGISTRATION NUMBER: 32,918

REFERENCE/DOCKET NUMBER: 1102:

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/
FILING DATE: 18-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 12-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
                                                                                                                        APPLICATION NUMBER: 19-JUN-FILING DATE: 19-JUN-PRIOR APPLICATION DATA: APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/00
FILING DATE: 15-APR-1997
CLASSIFICATION: 530
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APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
                                                                                                                                                                                            FILING DATE: 09-DEC-
PRIOR APPLICATION DATA:
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TOPOLOGY: linear
MOLECULE TYPE: protein
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LENGTH: 267 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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500 West Madison Street, 34th floor
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100.0%; Pred. No. 1.7e-78;
ative 0; Mismatches 0;
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                                    11022US09/200-70.P3.C3
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NITMEDEN. ...
                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/646,360
FILING DATE: 13-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Carroll, Stephen F. APPLICANT: Studnika, Gary M.
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                                                                                                            PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                        APPLICATION NUMBER: US 07/901,707 FILING DATE: 19-JUN-1992
                                                                                                                                                                               APPLICATION NUMBER: US 08/064,691 FILING DATE: 12-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Chicago
                                                                                                                             APPLICATION NUMBER: FILING DATE: 09-DEC
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                                                                                                                     NUMBER: US 07/988,430
09-DEC-1992
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; MOLECULE TYPE: protein US-09-136-389-1
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US-09-610-838-1
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Best Local Similarity
                            PRIOR APPLICATION UMBER: US 08/064,691
APPLICATION UMBER: US 07/988.430
FILING DATE: 09-DEC-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
                                                                                                                                APPLICATION NUMBER: PCT/US94/05348 FILING DATE: 12-MAY-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunoto
TITLE OF INVENTION: Proteins
                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/610,838
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 312/, ...
TELEFAX: 650 388-1248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                   APPLICATION NUMBER: 08/64 FILING DATE: 13-MAY-1996
                                                                                                                                                                                                                     APPLICATION NUMBER: US/0 FILING DATE: 18-AUG-1998
                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
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500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
UMBER: US 07/901,707
19-JUN-1992
                                                                                                                                                                                                                                                                                        06-JUL-2000
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173
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PCT-US92-09487-1
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Best Local Similarity
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TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
     FILING DATE: 19-JUN-1552
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/787,567
                                                          CLASSIFICATION:
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: US 07/901,707
                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Materials Comprising and Methods of TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins
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TOPOLOGY: linear
MOLECULE TYPE: protein
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
                                                APPLICATION NUMBER: US 07 FILING DATE: 19-JUN-1992
                                                                                                                            APPLICATION NUMBER: FILING DATE: 19921
APPLICATION NUMBER: US CFILING DATE: 04-NOV-1991
                                                                                                                                                                                                                                                                                                                                            STREET: Two First National Plaza, 20 South Clark STREET: Street
                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                           CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
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Lei, Shau-Ping
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Carroll, Stephen F.
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                                                                                                                                            PCT/US92/09487
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TELEFAX: (314, 1 TELEFAX: 25-8856
TELEX: 25-8856
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 267 amino acids TYPE: AMINO ACID
TYPE: AMINO ACID
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Best Local S
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               TELEFAX: (617) 248-71(
INFORMATION FOR SEQ ID NO:
                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/831,967
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                               COMPUTER: IBM PC COmpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Biosynt
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REGISTRATION NUMBER: 35302
REFERENCE, DOCKET NUMBER: 31:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                             REFERENCE/DOCKET NUMBER: CR
                                                                                              NAME: Pitcher, Edmund REGISTRATION NUMBER: 2
                                                                                                                                                                                                  CLASSIFICATION: 424
                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                     STATE:
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5877305
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                                                                                                                                                                                                                                                                                                                                                                                  Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                 Exchange Place, 53 State Street
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Houston, L. L.
                                                                                                                                                                                                                                                                                                                                                                  USA
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                                                                                                                                                                                                                                                                                                             Floppy disk
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100.0%;
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; Pred. No. 1.7e-78;
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                                                                                                                        ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-356-786-10
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US-08-356-786-10
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                                        Query Match 78.9%; Score 748; DB 2; 1
Best Local Similarity 100.0%; Pred. No. 4.5e-78;
Matches 144; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION: APPLICANT: Huston
                                                                                                                                                                                                  TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 534 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/831,967
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer TITLE OF INVENTION: Marker NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                  NAME: Pitcher, Edmund R.
REGISTRATION NUMBER: 27,829
REFERENCE/DOCKET NUMBER: CRP-053
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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    36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 95
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                                                                                                                                                                                   amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Edmund R. Pitcher, Testa, Hurwitz, & Thibeault Exchange Place, 53 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Houston, L. L.
Ring, David B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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                                                                              Length 534;
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                                              Indels
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     156 GNYDRLEQLAGNLRENIELGNGPL 179
124 GNYDRLEQLAGNLRENIELGNGPL 147
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search completed: September 16, 2003, 11:51:46
Job time: 11.1972 secs

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Result
No.
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OM protein - protein search, using sw model
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204.5
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       Query
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                                                                                                                                                                                                                                                                                                                                        : /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*

1: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*

1: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*

1: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgn2_6/picodata/2/pubpaa/US06_HEW_PUB.pep:*
/cgn2_6/picodata/2/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/picodata/2/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/picodata/2/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/picodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
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US-09-347-064-2
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US-10-282-935-1

US-09-792-7938-39

US-10-127-890-6

US-10-127-890-6

US-10-280-6798-4

US-10-282-935-3

US-09-792-7938-34
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                 US-10-127-890-7
US-10-127-890-5
US-10-127-890-110
US-10-127-890-111
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1439.723 Million cell updates/sec
           Sequence 1, Appli
Sequence 39, Appli
Sequence 6, Appli
Sequence 4, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 8, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 110, App
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Sequence
Sequence
    101,
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US-10-127-890-1
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259	332	330	332	280	280	280	280	263	154	250	250	261	314	251	332	309	293	251	251	251	251	251	251	251	251	251	251	251	
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## ALIGNMENTS

Sequence 1, Application US/10/27890
Publication No. US20030166196A1
GENERAL INFORMATION:

APPLICANT: Better, Marc D.
Carroll, Stephen F.
Carroll, Stephen F.
Studnika, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 173

CORRESPONDENCE ADDRESS:
ADDRESSE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZUMBER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER REALABLE FORM:
MEDIUM TYPE: Patentin Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1994
APPLICATION NUMBER: US/08/646,360
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 07/988,430
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 19-JUN-1992

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                                                                                                                                                                                                                                                                                                           FILE REFERENCE: UTSD:884US
CURRENT APPLICATION NUMBER: US/10/282,935
CURRENT FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: 09/538,873
PRIOR FILING DATE: 2000-03-30
PRIOR FILING DATE: 1999-03-30
PRIOR FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.1
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Publication No. US20030143193A1
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Best Local Similarity
                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                               SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: BALUNA, ROXANA G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
TITLE OF INVENTION: PROTEINACEOUS COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: SMALLSHAW, JOAN APPLICANT: BALUNA, ROXANA G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: VITETTA, ELLEN S. APPLICANT: GHETIE, VICTOR F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 650 388-1248 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Peptide
                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/787,567 FILING DATE: 04-NOV-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                      ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                                                    142;
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      1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: McNicholas, Janet M. REGISTRATION NUMBER: 32,918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 267 amino acids TYPE: amino acid
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                                                                                  Conservative
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; Pred. No. 6.8e-76;
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                                                                                                      score 738; DB 12;
pred. No. 9.1e-75;
                                                                                    Mismatches
                                                                                                                        Length 267;
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I ENGTH: 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/10127890 Publication No. US20030166196A1 GENERAL INFORMATION:
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APPLICANT: Coggins, Philip
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
FILE REFERENCE: 25020-601D
FILE REFERENCE: 25020-601D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/792,793A
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 93
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Trichosanthews kirilowii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Better, Marc D.
Carroll, Stephen F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  123 YDRLEQLAGNLRENIELGNGPL 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104 SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDA-EAITHLETDVQNRYTFAFGGNYDRLE 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 INFTTAGATYQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 103
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56; Conserv
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                                                                         COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                     STREET: 500 We
CITY: Chicago
                APPLICATION NUMBER: US/10/127,890 FILING DATE: 23-Apr-2002
                                                                                                                                                                                               COUNTRY: USA
                                                                                                                                                                                                                  STATE: Illinois
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                           ADDRESSEE: McAndrews, Held & Malloy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                          500 West Madison Street,
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Publication No. US20030150019A1
GENERAL INFORMATION:
APPLICANT: Large Scale Biology Corporation
TITLE OF INVENTION: Monopartite RNA Virus Transformation Vectors
FILE REFERENCE: LSBC-0109-US93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                         PRIOR FILING DATE: 1990-10-22
PRIOR APPLICATION NUMBER: 07/641,617
PRIOR FILING DATE: 1991-01-16
PRIOR APPLICATION NUMBER: 07/737,899
PRIOR FILING DATE: 1991-07-26
                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/280,679B CURRENT FILING DATE: 2000-10-24 PRIOR APPLICATION NUMBER: 09/557,941 PRIOR FILING DATE: 2000-04-24
                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 08/484,341 PRIOR FILING DATE: 1995-06-07
                                                                                                                                                                                                                  PRIOR FILING DATE: 1992-07-31
PRIOR APPLICATION NUMBER: 07/600,244
                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 07/923,692
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               APPLICATION NUMBER: 07/739,143
FILING DATE: 1991-08-01
APPLICATION NUMBER: 07/3310,881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: MCNICHOLAS, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
FILING DATE: 1989-02-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protei
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LENGTH: 247 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116 TAAGKIRENIPLG 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VSFRLSGATSSSYGVFISNLRKALPNERKL-YDIPLL--RSSLPGSQRYALIHLTNYADE 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/787,567 FILING DATE: 04-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07
FILING DATE: 19-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/064,691 FILING DATE: 12-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/988,430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US 07/901,707
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Sequence 3, Application US/10282935
Publication No. US20030143193A1
GENERAL INFORMATION:
APPLICANT: VITETTA, ELLEN S.
APPLICANT: GHETIE, VICTOR F.
APPLICANT: SMALLSHAW, JOAN
APPLICANT: BALUNA, ROXANA G.
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; TYPE: PAT
; ORGANIZM: Chinese cucumber protein alpha-trichosanthin
US-10-280-679B-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/126,826
PRIOR FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3
                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                               Query Match
Best Local :
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Best Local :
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS
TITLE OF INVENTION: PROTEINACEOUS COMPOUNDS
FILE REFERENCE: UTSD:884US
CURRENT APPLICATION NUMBER: US/10/282,935
CURRENT FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: 09/538,873
PRIOR FILING DATE: 2000-03-30
PRIOR FILING DATE: 2000-03-30
PRIOR FILING DATE: 2000-03-30
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TYPE: PRT
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PRIOR FILING DATE: 1988-02-26
PRIOR APPLICATION NUMBER: 07/160,771
PRIOR FILING DATE: 1988-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28.0%; Score 265.5; DB 1
Local Similarity 42.1%; Pred. No. 1.6e-21;
les 56; Conservative 32; Mismatches 38
117 ERWAHQSRQQIPLG 130
                                                                                                                                104 SYTLALDYTNAYYVGYRAGNSAYFFH--PDNQEDAEAITHLFTDVQNRYTFAFGGNYDRL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              163 QLAGNLRENIELG 175
                                                                                   63 SIEVGIDVTNAYVVAYRAGTQSYFLRDAPSSASD----YLFTGT-DQHSLPFYGTYGDL
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                                                                                                                                                                           5 IKFSTEGATSQSYKQFIEALRERLRGG--LIHDIPVLPDPTTLQERNRYITVELSNSDTE
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                                        EQLAGNLRENIELG 175
                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                             25.8%;
                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                                             Score 245; DB 12;
Pred. No. 2.6e-19;
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TYPE: PRT
; ORGANIEM: Bryonia dioica
US-09-792-793A-34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
US-09-792-793A-34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/792,793A CURRENT FILING DATE: 2001-02-22 NUMBER OF SEQ ID NOS: 93
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 34
LENGTH: 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 34, Application US/09792793A Patent No. US20020168370A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/10127890 Publication No. US20030166196A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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APPLICANT: Coggins, Philip
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
FILE REFERENCE: 25020-601D
                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Better, Marc D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              116 TAAGKIRENIPLG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          163 QLAGNLRENIELG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           104 SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 TISVAVDVTNVYIMGYLAGDVSYFF---NEASATEAAKFVFKDAKKKVTLPYSGNYERLQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 VSFRLSGATTTSYGVFIKNLREALPYERKV-YNIPLL--RSSISGSGRYTLLHLTNYADE 58
APPLICATION NUMBER: US 08/064,691 FILING DATE: 12-MAY-1993 APPLICATION NUMBER: US 07/988,430 FILING DATE: 09-DEC-1992
                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Chicago
STATE: Illinois
                                                                                                 APPLICATION NUMBER: PCT/US94/05348 FILING DATE: 12-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
                                                                                                                                                  APPLICATION NUMBER: US/08/646,360 FILING DATE: 13-MAY-1996
                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: McAndrews, Held & Malloy, Ltd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Carroll, Stephen F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24.9%; Score 236.5; DB 10; 39.8%; Pred. No. 2.3e-18; ative 31; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proteins
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106 TLALDYTNAYYVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLA 165

THQTTGEEYFRFITLLRDYVSSGS-FSNEIPLL-RQSTIPVSDAQRFVLVELTNQGGDSI

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US-09-347-064-2
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                                                                                                                                                                                               SEQ ID NO 2
LENGTH: 252
                                             Matches
                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. US20020045208A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09347064A
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                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 09282-5
CURRENT APPLICATION NUMBER: US/09/347,064A
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: PCT/EP98/00009
EARLIER FILING DATE: 1998-01-02
EARLIER APPLICATION NUMBER: EP 97 10 0012.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Eck, Jurgen APPLICANT: Schmidt, Arno APPLICANT: Zinke, Holger
                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Recombinant Fusion Proteins Based on TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe Viscum TITLE OF INVENTION: Album
                                                                                                                                                                                                                                          SOFTWARE: Patentin Ver.
                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                 EARLIER FILING DATE: 1997-01-02
                                                                                                                                                    ORGANISM: Viscum album
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 4:
                                             Local Similarity
Les 55; Conserv
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TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 07/787,567 FILING DATE: 04-NOV-1991 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             115 AAHKIRENIDLG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      164 LAGNLRENIELG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQ 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 TISVAIDVTNVYVVAYRTRDVSYFF---KESPPEAYNILFKGTR-KITLPYTGNYENLQT 114
48 TAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPIN--QRFILVELSNHAELSV 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: MCNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 19-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear ULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07/901,707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 263 amino acids
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                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arno
                                                               21.8%; Score 206.5; DB 9; 42.3%; Pred. No. 5.7e-15;
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                                           24; Mismatches
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Pred. No. 2.2e-15;
1; Mismatches 45
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                                               42;
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                                                                                        Length 252;
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US-10-127-890-7
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US-09-347-064-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/347,064A CURRENT FILING DATE: 1999-07-02 EARLIER APPLICATION NUMBER: PCT/EP98/00009 EARLIER FILING DATE: 1998-01-02 EARLIER APPLICATION NUMBER: EP 97 10 0012.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Eck, Jurgen
APPLICANT: Schmidt, Arno
APPLICANT: Both Anno
FITTLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe Viscum
TITLE OF INVENTION: album
FILE REFERENCE: 09282-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EARLIER FILING DATE: 1997-01-02 NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
         ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Better, Marc D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 GH-RDQIPLG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106 TLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 166 GNLRENIELG 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 TAAIDVTNLYVVAYQAGDQSYFLR-DAPRGAE--THLFTGT-TRSSLPFNGSYPDLERYA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48 TAGATVOSYTNEIRAVRGRLTTGADVRHEIPVLPNRVGLPIN--QRFILVELSNHAELSV 105
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55; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  252
                                                                                                                                          CITY: Chicago
STATE: Illinois
                                                                                                                          COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.8%; Score 206.5; DB 9; ilarity 42.3%; Pred. No. 5.7e-15; Conservative 24; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                      Carroll, Stephen F.
                                                                                                                                                                                                                                                                                                                 Studnika, Gary M.
                                                                                                                                                                                                                                                                        Proteins
                                                                                                                                                                                                                                                                                        Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 252;
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US-10-127-890-5
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 650 388-1248 INFORMATION FOR SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
ZIP: 60661

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd
                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 173
                                                                                                                                                                                                                                                      TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                          APPLICANT: Better, Marc D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 QIAAGKPREKIPIG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162 EQLAGNLRENIELG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103 LSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAE-AITHLFTDVQNRYTFAFGGNYDRL 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 KTITVAVDVTNVYIMGYLADTTSYFF---NEPAAELASQYVERDARKITLPYSGNYERL 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44 INFTTAGATYQSYTNFIRAVRGRLTTGADVRHEIP-VLPNRVGLPINQRFILVELSNHAE 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 VSFRLSGADPRSYGMFIKDLRNALPFREKV-YNIPLLLPSVSGA---GRYLLMHLFNYDG 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
                                                                                   STREET: 500 West
CITY: Chicago
STATE: Illinois
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 263 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 312/707-9155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: McNicholas, Janet M. REGISTRATION NUMBER: 32,91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/646,360 FILING DATE: 13-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                               Studnika, Gary M.
                                                                                                                                                                                                                                                                                                      Carroll, Stephen F.
                                                                                                                                                500 West Madison Street, 34th floor
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  compatible
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DB 12; Length 263;

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US-10-127-890-110
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TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 5:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: MCNicholas, Janet M.
REGISTRATION NUMBER: 32,918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 5:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                     CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                   TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                              APPLICANT: Better, Marc D.
Carroll, Stephen F.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 103
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APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
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CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US94/05348 FILING DATE: 12-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/646,360 FILING DATE: 13-MAY-1996
                                                                                        CITY: Chicago
STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 08/064,691
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                                                                     COUNTRY: USA
                                          ZIP: 60661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 248 amino acids
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                                                                                                                                                                                                                                Proteins
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US-10-127-890-111
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INFORMATION FOR SEQ ID NO: 110:
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CURRENT APPLICATION DATA:
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                                                                                                                       CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor
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       COMPUTER READABLE FORM
                                                                                                                                                                                            NUMBER OF SEQUENCES: 173
                                                                                                                                                                                                                                    TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                             APPLICANT: Better, Marc D. Carroll, Stephen F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 LE---GEKAYRETTDLGIEPL 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104 SVTLALDVTNAYVVGYRAGNSAYFFH--PDNQEDAEAITHLFTD-VQNRYTFAFGGNYDR 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161 LEQLAGN--LRENIELGNGPL 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL
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                                               CITY: Chicago
STATE: Illinois
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 251 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
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                                                                                                                                                                                                                 Proteins
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Indels 17;

Gaps

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RESULT 15
US-10-127-890-101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: amino acid; TOPOLOGY: linear; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 111: US-10-127-890-111
                                                                                                                                                                                                                                                                 Sequence 101, Application US/10127890 Publication No. US20030166196A1 GENERAL INFORMATION:
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
                                                                                                                                                                                                                        APPLICANT: Better, Marc D.
Carroll, Stephen F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: 312/707-8889
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                                                                                                                     CORRESPONDENCE ADDRESS
                                                                                                                                                                               TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 LE---GEKAYRETTDLGIEPL 133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 VSFSTCGATYITYVNFLNELRVKLKPEGN-SHGIPLLRKKADDP-GKAFVLVALSNDNGQ 62
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               STREET: 500 West
CITY: Chicago
STATE: Illinois
COUNTRY: USA
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FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
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APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
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ZIP: 60661
                                                                           ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
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                                                                                                                                                                                                   Studnika, Gary M.
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Search completed: September 16, 2003, 12:09:55 Job time: 19.5118 secs
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TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: MCNICHOLAS, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                              116
                                                                                                                                         161 LEQLAGN--LRENIELGNGPL 179
                                                                                                                                                                                                                                       104 SVTLALDVTNAYVVGYRAGNSAYFFH--PDNQEDAEAITHLFTD-VQNRYTFAFGGNYDR 160
                                                                                                                                                                                            63 LAEIAIDVTSVYVVGYQVRNRSYFFKDAPD-----AAYEGLFKNTIKTR--LHFGGSYPS 115
                                                                                                                                                                                                                                                                                                                                        44 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 103
                                                                                                                                                                                                                                                                                                                                                                                        ch 18.6%; Sc
l Similarity 37.6%; Pr
53; Conservative 22;
                                                                                                                                                                                                                                                                                     5 VSFSTKGATYITYVNFLNELRVKLKPEGN-SHGIPLLRKKADDP-GKAFVLVALSNDNGQ
                                                                                           LE---GEKAYRETTDLGIEPL 133
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 08/064,691 FILING DATE: 12-MAY-1993 APPLICATION NUMBER: US 07/988,430 FILING DATE: 09-DEC-1992 APPLICATION NUMBER: US 07/901,707 FILING DATE: 19-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: <Unknown>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/787,567 FILING DATE: 04-NOV-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 251 amino acids
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Copyright (c) 1993 - 2003 Compu
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## ALIGNMENTS

N:Contains: rRNA N-glycosidase (EC 3.2.2.2)
C;Species: Ricinus communis (castor bean)
C;Date: 31-Dec-1993 \*sequence\_revision 31-Dec-1993 \*text\_change 16-Jul-1999
C;Accession: A24041; S20513; A24614; A03372; A24010; A03374; S10903
R;Halling, K.C.; Halling, A.C.; Murray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F.
Nucleic Acids Res. 13, 8019-8033, 1985
A;Title: Genomic cloning and characterization of a ricin gene from Ricinus communis.
A;Reference number: A24041; MUID:86067214; PMID:2999712
A;Accession: A24041

ricin D precursor - castor bean

A; Molecule type: DNA A; Residues: 1-576 <HAL>

A; Cross-references: GB: X03179; NID: g21082; PIDN: CAA26939.1; PID: g21083

communis: cloning of a functional ricin ge  ${\tt PMID:1371405}$ 

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A;Molecule type: mRNA
A;Residues: 12-75,'D',77-550,'R',552-576 <LAM>
A;Residues: 12-75,'D',77-550,'R',552-576
A;Cross-references: GB:X02388; NID:g21077; PIDN:CAA26230.1; PID:g21078
A;YOShitake, S.; Funatsu, G.; Funatsu, M.
Agric. Biol. Chem. 42, 1267-1274, 1978
A;Title: Isolation and sequences of peptic peptides, and the complete sequence of Ile
A;Reference number: A03372
A;Accession: A03372
                                                                                             A;Molecule type: protein
A;Residues: 315-383,'PS',386-576 <ARA>
R;Funatsu, G.; Kimura, M.; Funatsu, M.
Agric. Biol. Chem. 43, 2221-2224, 1979
A;Title: Primary structure of Ala chair
                                                                                                                                                                                                                                                                                           A; Molecule type: protein
A; Residues: 36-97, (2/99-109,'S',111-269,'D',272-283,'L',285-288,290-302
A; Note: this paper cites the others in the series providing experimental a; R; Araki, T.; Funatsu, G.
FEBS Lett. 191, 121-124, 1985
A; Title: Revised amino acid sequence of the B-chain of ricin D due to los
A; Reference number: A24010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X52908; NID:g21084; PIDN:CAA37095.1; PID:g21085 R;Lamb, F.I.; Roberts, L.M.; Lord, J.M. Eur. J. Biochem. 148, 265-270, 1985 Eur. J. Biochem. 148, 265-270, 1985 A;Title: Nucleotide sequence of cloned cDNA coding for preproricin. A;Reference number: A24614; MUID:85179479; PMID:3838723 A;Accession: A24614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R:Tregear, J.W.; Roberts, L.M.
Plant Mol. Biol. 18, 515-525, 1992
A:Title: The lectin gene family of Ricinus
A;Reference number: S20513; MUID:92163016;
A;Accession: S20513
                                A; Reference number: A; Accession: A03374
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A; Residues: 1-576 <TRE>
A; Molecule type: protein
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A;Contents: annotation; X-ray crystallography, 2.5 angstroms
R;Katzin, B.J.; Collins, E.J.; Robertus, J.D.
Proteins 10, 251-259, 1991
A;Title: Structure of ricin A-chain at 2.5 angstroms.
A;Title: Structure of ricin A-chain at 2.5 angstroms.
A;Title: Structure of ricin A-chain at 2.5 angstroms.
A;Contents: annotation; X-ray crystallography, 2.5 angstroms
C;Comment: The functional molecule is a disulfide-linked dimer of A and B chains, which
C;Comment: The A chain inhibits protein synthesis; it inactivates the 60S ribosomal subunto the cell of the A chain; B chains are also responsible for cell agglutination (lectic) comment: This protein is cytotoxic and very poissonous to animals.
C;Comment: Trix ricin; rRNA relycosidase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C:Keywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed F;1-35/Domain: signal sequence *stratus predicted <SIG>F;1-35/Domain: ricin D chain A *status experimental <ACH>F;36-302/Product: ricin D chain B *status experimental <ACH>F;46-293/Domain: rRNA N-glycosidase homology <RNG>F;315-576/Product: ricin D chain B *status experimental <BCH>F;313-373,374-414,417-455,462-497,501-540,543-576/Region: 40-residue repeats F;45,409,449/Binding site: carbohydrate (Asn) (covalent) *status experimental F;15,158,243,244/Binding site: substrate (Tyr, Tyr, Glu, Asn) *status predicted F;112/Active site: Glu *status experimental F;215/Active site: Arg *status experimental F;215/Active site: Arg *status experimental F;216-Active site: Arg *status experimental F;316-3649,360/Binding site: N-acetylgalactosamine (Asp, Glu, Asn) *status experimental F;316-3649,360/Binding site: N-
                                                                                                                                                                                                                                                                                                       R;Roberts, L.M.; Lamb, I.F.; Pappin, D.J.C.; Lord, J.M.
J. Biol. Chem. 260, 15682-15686, 1985
A;Title: The primary sequence of Ricinus communis agglutinin.
A;Reference number: A24261; MUID:86059449; PMID:2999130
A;Accession: A24261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N;Contains: rRNA N-glycosidase (EC 3.2.2.2)
C;Species: Ricinus communis (castor bean)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C;Accession: A24261; A24210
                                        A;Cross-references: GB:M12089; NID:g169700; R;Araki, T.; Yoshioka, Y.; Funatsu, G. Biochim. Biophys. Acta 872, 277-285, 1986 A;Title: The complete amino acid sequence o:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Contents: annotation; active site R;Rutenber, E.; Robertus, J.D. Proteins 10, 260-269, 1991 Proteins 10, 260-269, 1991 A;Title: Structure of ricin B-chain at 2.5 angstrom resolution. A;Reference number: A48238; MUID:91352005; PMID:1881882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Note: this paper, one of a series, summarizes the experimental details for the determine R;Ready, M.P.; Kim, Y.; Robertus, J.D.

Proteins 10, 270-278, 1991
     A; Reference
                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-564 < ROB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Residues: 315-335,'N',337-342,'NH',345-362,364-383,'PS',386-399,'T',401,'D',403,'E',40527,'E',529-564,'W',566,'H',567-570,'LI',573-574,'F' <FUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;548,569/Binding site: N-acetylgalactosamine (Asp, Asn) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      179;
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     number: A24210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Н
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYR 120
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No. 1.4e-78;
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                                                  of the B-chain
                                                                                                                                                                                         PIDN: AAA33869.1; PID: g16970
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                                             of the Ricinus communis aggluti
                                                                                                                                                                                                                                                                                                                                                                                                                               Comparison with ricin.
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A;Title: Preproabrin: genomic cloning, characterisation A;Reference number: S16022; MUID:91266957; PMID:2050149 A;Accession: S16022
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C;Comment: Abrin consists of an A chain, which inhibits protein synthesis by inactiva
The A and B chains are linked by a single disulfide bond, which is essential for tox
C;Superfamily: ricin; rRNA.N-glycosidase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N;Contains: rRNA N-glycosidase (EC 3.2.2.22)
C;Species: Abrus precatorius (Indian licorice)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;324,337,348/Binding site: N-acetylgalactosamine (Asp, Gln, Asn) *status predicted F;397,437/Binding site: carbohydrate (Asn) (covalent) *status experimental F;536,557/Binding site: N-acetylgalactosamine (Asp, Asn) *status predicted
                                                                      F;534,555/Binding site: N-acetylgalactosamine (Asp, Asn) #status
                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-562 < WOO>
                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
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   Matches
                                      Query Match
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                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72 DVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPD
71;
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93.5%;
                     44.18;
                                    30.1%;
   18;
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                   Score 285; DB 2;
Pred. No. 3.9e-18;
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     Mismatches
                                                                                                                                                     Tyr, Glu, Asn) #status predicted

3d
                                  Length 562
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     Indels
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19 LCFGSTSGWSFTLEDNNIFP-----KQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVR 74

PID:g166297

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A;Cross-recterences: GB:M98346
C;Comment: Abrin consists of an A chain, which inhibits protein synthesis by inactivating C;Comment: Abrin consists of an A chain, which inhibits protein synthesis by inactivating The A and B chains are linked by a single disulfide bond, which is essential for toxicing C;Superfamily: ricin rRNA N-glycosidase homology
C;Reywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin; F;1-251/Product: abrin-d chain A #status predicted <ACH>F;1-251/Product: abrin-d chain B #status predicted <ACH>F;261-528/Product: abrin-d chain B #status predicted <BCH>F;283-325,326-336,369-407,414-449,453-492.495-528/Region: 40-residue repeats F;1/Modified site: pyrrolidone carboxylic acid (GIn) #status predicted F;41-13,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted F;200,253,361,401,402/Binding site: carbohydrate (Asn) (covalent) #status predicted F;207-269,286-305,329-346,417-430,456-473/Disulfide bonds: #status predicted F;208,312/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted F;208,312/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
                      abrin-b precursor - Indian licorice (fragment)
N;Contains: rRNA N-glycosidase (EC 3.2.2.2)
C;Species: Abrus precatorius (Indian licorice)
C;Date: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 20-Aug-1999
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S32430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R:Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
J. Mol. Biol. 229, 263-267, 1993
A;Title: Primary structure of three distinct isoabrins determined by cDNA sequencing. Cq
A;Reference number: S32429; MUID:93132798; PMID:8421313
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C;Species: Abrus precatorius (Indian licorice)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                abrin-d precursor - Indian licorice (fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                 115 DLERWAHQTREEISLG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 HAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYD 159
                                                                                                                                                                                                                                                                                                                                                                                                     160 RLEQLAGNLRENIELG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                          59 SERESIEVGIDYTNAYYVAYRAGSQSYFL---RDAPASASTYLFPGTQ-RYSLRFDGSYG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40 QYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSN 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QDQVIKFTTEGATSQSYKQFIEALRQRLTGG--LIHDIPVLPDPTTVEERNRYITVELSN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75 HEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQE 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1-528 <HUN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Pred. No. 6.8e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48; Indels
A;Molecule type: DNA
A;Residues: 1-233,'T',235-246,'M',248-289 <CHO>
A;Cross-references: GB:UU5434; NID:g170534; PIDN:AAA34206.1; PID:g170535
R;Zheng, H.G.; Wang, B.; Shao, P.Z.; Yang, X.R.
                                                                                                                                                                          A;Molecule type: mRNA
A;Residues: 1-289 <SHAY
A;Cross-references: GB:M34858; NID:g170536; PIDN:AAA34207.1; PID:g170537
A;Cross-references: GB:M34858; NID:g170536; PIDN:AAA34207.1; PID:g170537
A;Experimental source: tuber
R;Chow, T.P.; Feldman, R.A.; Lovett, M.; Piatak, M.
J. Biol. Chem. 265, 8670-8674, 1990
A;Title: Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a type I
A;Reference number: A36274; MUID:90256790; PMID:2341400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Experimental source: seed

C;Superfamily: ricin; rRNA N-glycosidase homology
C;Keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; l
F;1-250/product: abrin-b chain A #status predicted <aCH>
F;1-250/product: abrin-b chain B #status experimental <BCH>
F;260-527/Product: abrin-b chain B #status experimental <BCH>
F;282-343,325-365,368-406,413-448,452-491.494-527/Region: 40-residue repeats
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F;74,113,194,195/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F;110,360,400/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;163,166/Active site: Glu, Arg #status predicted
F;246-268,285-304,328-345,416-429,455-472/Disulfide bonds: #status predicted
F;248-311/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
F;499,520/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rRNA N-glycosidase (EC 3.2.2.2) alpha-trichosanthin precursor [validated] - Mongolia R;Alternate names: alpha-TCS; type I ribosome-inactivating protein C:Species: Trichosanthes kirilowii (Mongolian snake-gourd) C:Date: 30-Sep-1988 #sequence_revision 26-Jan-1996 #text_change 23-Mar-2001 C:Accession: JT0566; A36274; JC1093; A36273; JT0003 R:Shaw, P.C.; Yung, M.H.; Zhu, R.H.; Ho, W.K.K.; Ng, T.B.; Yeung, H.W. Gene 97, 267-272, 1991
A;Title: Cloning of trichosanthin cDNA and its expression in Escherichia coli.
                                                                                                                                                              A; Accession: A3627
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Blosci. Blotechnol. Blochem. 57, 166-169, 1993
A;Tille: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, to A;Reference number: JC1398; MUID:93169023; PMID:7763422
A;Accession: JC1399
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A;Residues: 260-281,'D',283-290,'N',292-349,'PQ',352-377,'N',379-425,'M',427,'D',429-
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A; Residues: 1-527 <HUN>
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J. Mol. Blol. 229, 263-267, 1993
A;Title: Primary structure of three distinct isoabrins determined by cDNA sequencing.
A;Reference number: S32429; MUID:93132798; PMID:8421313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 RLEQLAGNLRENIELG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 HAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYD 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59 SDTESIEAGIDVSNAYVVAYRAGNRSYFL---RDAPTSASRYLFTGTQ-QYSLRFNGSYI 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40 QYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSN 99
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47.8%; Pred. No. 1
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Gaps

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Acta Genet. Sin. 21, 42-51, 1994
A;TitLe: Cloning and DNA sequencing of the gene encoding Trichosanthin.
A;Reference number: JC1093; MUID:94271613; PMID:8003348
A;Accession: JC1093
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A;Title: Scientific evaluation of Tian Hua Fen (THF): history, chemistry and application A;Reference number: JT0003
A;Accession: JT0003
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A; Residues: 1-72, 'V',74-90, 'S',92-233, 'T',235-267,'D',269-289 <ZHE>
A; Residues: 1-72, 'V',74-90, 'S',92-233, 'T',235-267,'D',269-289 <ZHE>
A; Cross-references: GB:S70176; NID:9547148; PIDN:AAB31048.1; PID:9547149
A; Cross-references: GB:S70176; NID:9547148; PID:9547148; PID:9547149
A; Maintenances: GB:S70176; NID:9547148; PIDN:AAB31048.1; PID:9547149
A; Maintenances: GB:S70176; NID:9547148; PIDN:AAB31048.1; PID:9547149
A; Cross-references: GB:S70176; NID:9547148; PID:9547148; PID:9547148; PID:9547149
A; Cross-references: GB:S70176; NID:9547148; PID:9547148; PI
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A;Reference number: A36273; MUID:90256789; PMID:2341399
A;Accession: A36273
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N; Contains: rRNA
       abrin (clone 7.2) precursor - Indian licorice (fragment) N;Contains: rRNA N-glycosidase (EC 3.2.2.22)
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   N-glycosidase
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A; Accession: $14471
A; Molecule type: DNA
A; Residues: 'M', 1-251 <EV2>
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                                                                                       В
                                                                                                                                                         Qy
                                                                                                                                                                                                                               Вþ
                                                                                                                                                                                                                                                                                             Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 119 WAHQTREQISLG 130
                     163 QLAGNLRENIELG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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C;Species: Abrus precatorius (Indian licorice)
C;Date: 21-Feb-1992 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
C;Accession: C39761; S14471
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A;Residues: 1-251 <EVE>
A;Residues: 1-251 <EVE>
R;Evensen, G; Mathiesen, A.; Sundan, A.
submitted to the EMBL Data Library, October 1990
submitted to the EMBL Data Library October 1990
A;Description: Direct molecular cloning of two distinct abrin A-chains.
A;Description: Direct molecular cloning of two distinct abrin A-chains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Evensen, G.; Mathiesen, A.; Sundan, J. Biol. Chem. 266, 6848-6852, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     karasurin - Mongolian snake-gourd c;Species: Trichosanthes kirilowii (Mongolian snake-gourd) c;Species: Trichosanthes kirilowii (Mongolian snake-gourd) c;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 12-Apr-1995 c;Accession: JU0393; PS0163 R;Toyokawa, S; Takeda, T.; Kato, Y.; Wakabayashi, K.; Ogihara, Y. Chem. Pharm. Bull. 39, 1244-1249, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Note: a sequence which lacks Ala-247 is also shown in this publication C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology C;Keywords: abortifacient F;4-243/Domain: rRNA N-glycosidase homology <RNG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: The complete amino acid sequence of an abortifacient protein, karasurin. A;Reference number: JU0393; MUID:92005921; PMID:1914000 A;Accession: JU0393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104 SYTLALDYTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQ 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPYLPNRVGLPINQRFILVELSNHAEL 103
                                                                     104 SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 162
59 TISVAIDVTNVYVMGYRAGDTSYFF---NEASATEAAKYVFKDAKRKVTLPYSGNYERLQ
                                                                                                                                                                                                                         44 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL
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                                                                                                                                                   2 VSFRLSGATSSSYGVFISNLRKALPYERKL-YDIPLL--RSTLPGSQRYALIHLTNYADE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIEVGIDVTNAYVVAYRAGSQSYFL --- RDAPASASTYLFTGTQ-RYSLRFDGSYGDLER
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                                                                                                                                                                                                                                                                                                                                          27.6%;
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                                                                                                                                                                                                                                                                                                          32; Mismatches
                                                                                                                                                                                                                                                                                                                                                 Pred.
                                                                                                                                                                                                                                                                                                                                             Score 261.5; DB Pred. No. 2e-16;
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A;Molecule type: protein
A;Residues: 22-270 CKON>
A;Residues: 22-270 CKON>
C;Comment: This protein is a ribosome-inactivating protein and exhibit cytotoxic, C;Comment: This protein belongs to type I ribosomal-inactivating proteins which ca C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
E;22-270/product: karasurin C #status predicted C;32-270/product: karasurin A #status predicted C;42-270/product: karasurin A #status predicted C;27-266/Domain: rRNA N-glycosidase homology C;27-266/Domain: rRNA N-glycosidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: DDBJ:AB000666; NID:g2329830; PIDN:BAA21786.1; PID:g2329831 R;Kondo, T.; Mizukami, H.; Takeda, T.; Ogihara, Y. Biol. Pharm. Bull. 19, 1485-1489, 1996 A;Title: Amino acid sequences and ribosome-inactivating activities of karasurin-B and karasterince number: JC5032; MUID:97108848; PMID:8951169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C:Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 19-Jul-2002 C:Accession: JC5606; JC5038 R:Mizukami, H.; Iida, K.; Kondo, T.; Ogihara, Y. Biol. Pharm. Bull. 20, 711-713, 1997 A:Title: Cloning and bacterial expression of a gene encoding ribosome-inactivating prote A:Reference number: JC5606; MUID:97356562; PMID:9212998
                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-289 <MIZ>
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A;Molecule type: protein
A;Residues: 1-247 <KON>
C;Comment: This protein belongs to type I ribosomal-inactivating proteins which catalyti
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
F;4-243/Domain: rRNA N-glycosidase homology <RNG>
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A;Accession: JC5032
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C;Species: Trichosanthes kirilowii var. japonica
C;Daecies: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 23-May-1997
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                                                                                                                 Query Match
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                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 OLAGNLRENIELG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 IAAGKIRENIPLG 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 103
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                                                                                27.6%; Score 261.5; DB 2; 42.9%; Pred. No. 2.4e-16;
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Pred. No. 2e-16;
                                                  Mismatches
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                                              Indels
                                                                                                       Length 289;
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                                           7;
                                        Gaps
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                                        4.
                              A;Title: The complete primary structure of abrin-a B ch A;Reference number: S24133; MUID:92371656; PMID:1505674 A;Accession: S24133
                                                                                                                                                                                                                                                                                                                                                                  A:Molecule type: protein
A:Residues: 261-347,'T',349-351,'A',353-357,'L',359-528
A:Experimental source: seed
R:Evensen, G:: Mathiesen, A:: Sundan, A:
submitted to the EMBL Data Library, October 1990
A:Description: Direct molecular cloning of two distinct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Note: residues 1-8 were derived from the synthesized primer R;Kimura, M.; Sumlzawa, T.; Funatsu, G. Biosci. Biotechnol. Biochem. 57, 166-169, 1993
A;Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, A;Reference number: JC1398; MUID:93169023; PMID:7763422
   A; Molecule type:
                                                                                                                               FEBS Lett
                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 'ME', 2-251 <EV2>
                                                                                                                                                                                                                                                                                                                      A;Reference number: S14471
A;Accession: S14472
                                                                                                                                                                   R;Chen,
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A; Accession: JC1398
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A;Residues: 1-201,203-251 <FUN>
A;Residues: 1-201,203-251 <FUN>
A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore,
R;Evensen, G.; Mathiesen, A.; Sundan, A.
J. Biol. Chem. 266, 6848-6852, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:M98344; NID:g166294; PIDN:AAA32624.1; PID:g166295
A;Note: the coding region for the sequence shown is preceded by an ATG codon
A;Note: residues 1-8 were derived from the synthesized primer
R;Funatsu, G; Taguchi, Y.; Kamenosono, M.; Yanaka, M.
Agric. Biol. Chem. 52, 1095-1097, 1988
A;Title: The complete amino acid sequence of the A-chain of abrin-a, a toxic protein
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C.Sepcies: Abrus precatorius (Indian licorice)
C.Date: 31-Dec-1993 #sequence_revision 01-Aug-1997 #text_change 16-Jul-1999
C.Accession: S32429; JT0202; A39761; JC1398; S14472; S24133; S74110; S74111
R.Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
J. Mol. Biol. 229, 263-267, 193
A:Title: Primary structure of three distinct isoabrins determined by cDNA sequencing.
A:Reference number: S32429; MUID:93132798; PMID:8421313
                                                                                                                                                                                 A;Cross-references: EMBL:X54873; NID:g16090; PIDN:CAA38655.1; PID:g16091
                                                                                                                                                                                                                                                                                        A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Direct molecular cloning and expression of two distinct abrin A-chains A;Reference number: A39761; MUID:91201329; PMID:2016300 A;Accession: A39761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 'E', 2-251 <EVE>
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A; Accession: JT0202
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A; Residues: 'E', 2-528 <HUN>
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                                                                                                                           Y.L.; Chow, L.P.; Tsugita, A.; Lin, J.Y. 
tt. 309, 115-118, 1992
                                                                                                                                                                                                                                                                                        preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104 SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 162
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protein
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A; Residues: 262-297,'Y',299-426,'L',428-466,'P',468-482,'L',484-528 <CHE>
R; Lin, S.H.; Chow, L.P.; Chen, Y.L.; Liaw, Y.C.; Chen, J.K.; Lin, J.Y.
EUr. J. Biochem. 240, 564-569, 1996
A; Title: probing the domain structure of abrin-a by tryptic digestion.
A; Reference number: S74110; MUID:97008945; PMID:8856055
A; Accession: S74110
A; Molecule type: protein
A; Residues: 89-108:154-172 <LIN>
A; Essidues: 89-108:154-172 <LIN>
A; Essidues: 80-108:154-172 <LIN>
A; Rocession: S74111
A; Molecule type: protein
A; Residues: 262-276,'X',278-280;329-348;369-388;399-418 <LIW>
A; Residues: 262-276,'X',278-280;329-348;369-388;399-418 <LIW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Luffa cylindrica (smooth loofah)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 20-Aug-1999
C;Accession: S23519; S23113
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A;Title: Nucleotide sequence of cDNA encoding beta-luffin, another ribosome-inactivating A;Reference number: S23519; MUID:92353400; PMID:1643290
A;Accession: S23519;
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beta-luffin - smooth loofah
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A; Residues: 1-278 < KAT>
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104 SVTLALDVTNAYVVGYRAGNSAYFFH--PDNQEDAEAITHLFTDVQNRYTFAFGGNYDRL 161
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                                                         89 NQRFILVELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQN 148
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                                                                                                                                                                                                                                                     29 FTLEDNNIFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPI 88
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                                                                                                                                                       FTVEGAN-----VSFSLSGADSKSYSKFITALRKALPSKEKVSNIPLLLPSASGA-- 66
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                                                                                                                                                                                                                                                                                                                                                                                                       24.3%; Score 230; DB 2; Length 278; 35.4%; Pred. No. 1.7e-13;
     18; Mismatches
                                                                                                                                                                                                                                                                                                                                                             32; Mismatches
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RESULT 13
JN0108
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A; Accession: PD0018
A; Accession: PD0018
A; Mclecule type: protein
A; Residues: 1-254 < CESC>
C; Superfamily: ricin; rRNA N-glycosidase homology
F; 7-246/Domain: rRNA N-glycosidase homology < RNG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Islam, M.R.; Hirayama, H.; Funatsu, G. Agric. Biol. Chem. 55, 229-238, 1991
A;Title: Complete amino acid sequence of luffin-b, a ribosome-inactivating protein fr A;Teference number: JN0108; MUID:91248488; PMID:1368666
A;Accession: JN0108
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C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 07-May-1999
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R;Eschenburg, S.; Krauspenhaar, R.; Mikhailov, A.; Stoeva, S.; Betzel, C.; Voelter, W
R;Eschenburg, S.; Krauspenhaar, R.; Mikhailov, A.; Stoeva, S.; Betzel, C.; Voelter, W
Biochem. Biophys. Res. Commun. 247, 367-372, 1998
Biochem. Biophys. Res. Commun. 247, 367-372, 1998
A;Title: Primary structure and molecular modeling of mistletoe lectin I from Viscum a
A;Title: Primary structure. 247, 26726173, 2477-3642173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Viscum album
C;Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 26-Aug-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 AAGKIREKIPLG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164 LAGNLRENIELG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 SYTLALDYTNAYYVGYRAGNSAYFFHPDNQEDAEAITHLETDVQNRYTFAFGGNYDRLEQ 163
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  123 GH-RDQIPLG 131
                                                                                                                                                            106 TLALDYTNAYVYGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLA 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60 AITMAIDVTNVYIMGYLVNSTSYF---ANESDAKLASQYVFKGSTLVTIPYSGNYERLQN 116
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                                                         166 GNLRENIELG 175
                                                                                                         67 TAAIDVTNAYVVAYQAGDQSYFLR-DAPRGAE--THLFTGT-TRSSLPFNGSYPDLERYA 122
                                                                                                                                                                                                                                                                         48 TAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPIN--QRFILVELSNHAELSV 105
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                                                                                                                                                                                                                     9 THQTTGEEYFRFITLLRDYVSSGS-FSNEIPLL-RQSTIPVSDAQRFVLVELTNQGQDSV
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43.8%; Pred. No. 2.6
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rRNA N-glycosidase (EC 3.2.2.2) momordin II - balsam apple C;Species: Momordica balsamina (balsam apple) C;Date: 25-Feb-1994 #sequence_revision 03-Aug-1995 #text_change 20-Aug-1999 C;Accession: 25560 R;Ortigao, M.; Better, M.
Nucleic Acids Res. 20, 4662, 1992 A;Fille: Momordin II, a ribosome inactivating protein from Momordica balsamina, is homol A;Reference number: S2550; MUID:93027170; PMID:1408771 A;Accession: S2550 A;Status: preliminary A;Molecule type: mRNA A;Residues: preliminary A;Molecule type: mRNA A;Residues: 1-286 <ORT>
A;Cross-references: EMBL:Z12175; NID:g19525; PIDN:CAA78166.1; PID:g19526 C;KeyWords: glycosidase; hydrolase
C;KeyWords: glycosidase; hydrolase
F;27-264/Domain: rRNA N-glycosidase homology <RNG>
Search completed: September 16, 2003, 11:50:32 Job time: 11:6091 secs
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Best Local Similarity

Matches 49; Conserv
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                                                                                                138 AAHKIRENIDLG 149
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: September 16, 2003, 11:30:32; Search time 6.2752 Seconds (without alignments) 1341.437 Million cell updates/sec

Title:
Perfect score:
Sequence: US-10-083-336A-2 948

1 MKPGGNTIVIWMYAVATWLC......RLEQLAGNLRENIELGNGPL 179

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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saponaria	saponaria	59 saponaria	<b>5</b>	aeromonas	hordeum	hordeum v	zea mays	dianthus	zea mays	zea mays		mirabilis	P10297 phytolacca	phytolacca	trichosant	luffa cyli		gelonium		momord	81446 viscum	22851 luffa cv	33183 sambucus	5 bryoni	11140	8 trichos	4	989 triche	06077 abrus	28590 abrus pr	6750 ricinus	P02879 ricinus com	scription	

# ALIGNMENTS

RP RX	RR R R R R R R R R R R	RP RT RN	RA RT RL RN	RY RX RT RL	RY RX RT RT RL	RY RA	R 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	RESULT RICI_R ID R AC P DT 2 DT 1 DT 1 DE R DE (
REVIEW. MEDLINE-21480122; PubMed=11595634; Olsnes S., Kozlov J.V.;	CARBOHYDRATE-LINKAGE SITES, AND PARTIAL SEQUENCE. MEDLINE-90344223; PubMed=1368517; Kimura Y., Kusuoku H., Tada M., Takagi S., Funatsu G.; "Structural analyses of sugar chains from ricin A-chain variant."; Agric. Biol. Chem. 54:157-162(1990).	SEQUENCE OF 315-576. Funatsu G., Kimura M., Funatsu M.; Primary structure of Ala chain of ricin D."; Agric. Biol. Chem. 43:2221-2224(1979).	SEQUENCE OF 36-302.  YOSHITAKE S., Funatsu G., Funatsu M.;  Yoshitake S., Funatsu G., Funatsu M.;  Sequence of Ile chain of ricin-D.";  Agric. Biol. Chem. 42:1267-1274(1978).	SEQUENCE OF 12-576 FROM N.A. MEDILINE-85179479; PubMed-3838723; Lamb A., Roberts L.M., Lord J.M.; "Nucleotide sequence of cloned cDNA coding for preproricin."; Eur. J. Biochem. 148:265-270(1985).	SEQUENCE FROM N.A.  MEDILINE-92163016; PubMed-1371405;  Tregear J.W., Roberts L.M.;  Trelectin gene family of Ricinus communis: cloning of a functional ricin gene and three lectin pseudogenes.";  Plant Mol. Biol. 18:515-525(1992).	SEQUENCE FROM N.A.  MEDLIND-86067214; PubMed-2999712;  Halling K.C., Halling A.C., Murray E.E., Ladin B.F., Houston L.L.,  Weaver R.F.;  "Genomic cloning and characterization of a ricin gene from Ricinus  communis.";  Nucleic Acids Res. 13:8019-8033(1985).	Ricinus communis (Castor bean).  Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  eurosids I; Malpightales; Euphorbiaceae; Ricinus.  NCBI_TaxID=3988;	LT 1 RICCO RICI_RICCO STANDARD; PRT; 576 AA. P02879; P02880; 21-UUL-1986 (Rel. 01, Created) 13-AUG-1987 (Rel. 05, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) Ricin precursor [Contains: Ricin A chain (rRNA N-glycosidase) (EC 3.2.2.22); Ricin B Chain].

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Toxicon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             extent to plant cells. The A chain is responsible for inhibiting protein synthesis through the catalytic inactivation of 60S ribosomal subunits. It acts as a glycosidase that removes a specific adenine residue from an exposed loop of 28S ribosomal factors, the modified ribosomes are unable to support protein synthesis. The A chain can inactivate a few thousand ribosomes per minute, thus inactivating them faster than the cell can make new ones. A single A-chain molecule can therefore kill an animal cell. The B chain binds to cell receptors and facilitates the entry into the cell of the A chain; B chains are also responsible for cell agglutination (Lectin activity). It binds to beta-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mutagenesis and X-ray crystallography.";
Protein Eng. 5:775-779(1992).
-:- FUNCTION: Ricin is higly toxic to an
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Rutenber E., Robertus J.D.;
"Structure of ricin B-chain at 2.5-A resolution.";
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"Structure of ricin A-chain at 2.5 A.";
Proteins 10:251-259(1991).
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Rutenber E., Xuong N.H., Hamlin R., Robert
"The three-dimensional structure of ricin
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"Analysis of several key active site residues of ricin
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                                                                                                                             specific adenosine on the 28S rRNA.
SUBUNIT: Disulfide-linked dimer of A and B chains.
DOMAIN: The B chain is composed of two domains, each domain consists of 3 homologous subdomains (alpha, beta, gamma).
PTM: THE MAJOR A-CHAIN IS GIYCOSYLATED ONLY IN POSITION 45 AND RECEIVED AND A CHAIN IS GIYCOSYLATED ONLY IN POSITION 45 AND RECEIVED AND A CHAIN IS GIYCOSYLATED ONLY IN POSITION 45 AND RECEIVED AND A CHAIN IS GIYCOSYLATED ONLY IN POSITION 45 AND RECEIVED AND A CHAIN IS GIYCOSYLATED ONLY IN POSITION 45 AND A CHAIN IS GIYCOSYLATED ONLY IN POSITION 45 AND A CHAIN IS GIYCOSYLATED ONLY IN POSITION 45 AND A CHAIN IS GIYCOSYLATED ONLY IN POSITION 45 AND A CHAIN IS GIYCOSYLATED ONLY IN POSITION 45 AND A CHAIN IS GIYCOSYLATED ONLY IN POSITION 45 AND A CHAIN IS GIYCOSYLATED ONLY IN POSITION 45 AND A CHAIN IS GIYCOSYLATED ONLY IN POSITION 45 AND A CHAIN IS GIYCOSYLATED ONLY IN POSITION 45 AND A CHAIN IS GIYCOSYLATED ONLY IN POSITION 45 AND A CHAIN IS GIYCOSYLATED ONLY IN POSITION 45 AND A CHAIN IS GIYCOSYLATED ONLY IN POSITION 45 AND A CHAIN IS GIYCOSYLATED ONLY IN POSITION 45 AND A CHAIN IS GIYCOSYLATED ONLY IN POSITION 45 AND A CHAIN IS GIYCOSYLATED ONLY IN POSITION 45 AND A CHAIN IS GIYCOSYLATED ONLY IN POSITION 45 AND A CHAIN IS GIYCOSYLATED ONLY IN POSITION 45 AND A CHAIN IS GIYCOSYLATED ONLY IN POSITION 45 AND A CHAIN IS GIYCOSYLATED ONLY IN POSITION 45 AND A CHAIN IS GIYCOSYLATED ONLY IN POSITION 45 AND A CHAIN IS GIYCOSYLATED ONLY IN POSITION 45 AND A CHAIN IS GIYCOSYLATED ONLY IN POSITION 45 AND A CHAIN IS GIYCOSYLATED ONLY IN POSITION 45 AND A CHAIN IS GIYCOSYLATED ONLY IN POSITION 45 AND A CHAIN IS GIYCOSYLATED ONLY IN POSITION 45 AND A CHAIN IS GIYCOSYLATED ONLY IN POSITION A CHAIN IS GIYON A CHAIN IN POSITION A CHAIN A CHA
                                    MINOR A-CHAIN IS GLYCOSYLATED ALSO IN POSITION 271. SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME.
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This SWISS-PROT entry is copyright. It is produced through
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CAUTION: REF. 4 AND REF. 5 SEQUENCES HAVE A HIGH NUMBER OF CONFLICTS
WITH THE SEQUENCE TRANSLATED FROM DNA (REF.1, REF.2 AND REF.3).
DATABASE: NAME-protein Spotlight;
                            ween the Swiss Institute of Bioinformatics European Bioinformatics Institute. There a
                                                                                                                                          WWW-"http://www.expasy.org/spotlight/articles/sptlt031.html"
                                                                                                                                                                                   NOTE=Issue 31 of February 2003
non-profit institutions as long
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CARBOHYD CONFLICT CONFLICT STRAND DISULFID DISULFID DISULFID PDB; PDB; PDB; PDB; PDB; PDB; PDB; ACT\_SITE REPEAT REPEAT PROSITE; PS50231; RICIN\_B\_LECTIN; 2.
PROSITE; PS00275; SHIGA\_RICIN; 1.
Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat; EMBL; REPEAT CHAIN PRINTS; GlycoSuiteDB; P02879; InterPro; IPR000772; I InterPro; IPR001574; I EMBL; CARBOHYD CARBOHYD REPEAT DOMAIN DOMAIN Plant defense; CARBOHYD REPEAT REPEAT DISULFID 1APG; 31-JAN-94.

1IFM; 31-QCT-93.

1IFF; 14-JAN-98.

1IFT; 14-JAN-98.

1IFT; 14-JAN-98.

1IFT; 16-JUN-97.

10BS; 16-JUN-97.

10BS; 16-JUN-97.

11BR5; 02-SEP-98.

11BR5; 02-SEP-98.

11L4; 16-JAN-02.

11L4; 16-JAN-02.

11L4; 16-JAN-02. PF00161; PF00652; Ricin\_ SM00458; RICIN; 2. PR00396; 14-JAN-98. 14-JAN-98. 31-OCT-93. 16-JUN-97. 31-JAN-94. 36 303 315 321 321 374 417 462 501 212 212 334 465 377 449 449 551 43 RLCSD 271 CAA26230.1; CAA01058.1; RIP; SHIGARICIN. Ricin\_B\_lectin RIP. B\_lectin; Signal; LINKER PEPTIDE.
RICIN B CHAIN.
RICIN B-TYPE LECTIN 1
RICIN B-TYPE LECTIN 2 RICIN B-T 2-ALPHA. RICIN A CHAIN 2-GAMMA. 1-BETA. INTERCHAIN 3D-structure -GAMMA 6 .) (IN MINOR FORM)

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RESULT 2
AGGL_RICCO
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Best Local Similarity
                                                                                                                                                                                                                                                  *Purification and physicochemical properties of ricins and agglutinins from Ricinus communis.";
Eur. J. Biochem. 105:453-459(1980).
-i- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28s ran.
-i- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
-i- SIMILARITY: Contains 2 ricin B-type lectin domains.
                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/
                   HSSP; P02879; 1BR6.
GlycoSuiteDB; P06750;
                                                    EMBL; M12089; AAA33869.1;
EMBL; S40368; AAB22584.1;
PIR; A24261; RLCSAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Agglutinin precursor (RCA) [Contains: Agglutinin glycosidase) (EC 3.2.2.22); Agglutinin B chain],
Ricinus communis (Castor bean).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Araki T., Yoshioka Y., Funatsu G.;
"The complete amino acid sequence of the B-chain of the Ricinus communis agglutinin isolated from large-grain castor bean seeds. Biochim. Biophys. Acta 872:277-285(1986).
                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=80178723; PubMed=6768555;
Lin T.T.-S., Li S.S.-L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 303-337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-86059449; PubMed=2999130;
Roberts L.M., Lamb F.I., Pappin D.J.C., Lord J.M.;
"The primary sequence of Ricinus communis agglutinin. Comparison with ricin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core e
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                                                                                                                      an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPL
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IPR000772; Ricin_B_lectin
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Pred. No. 1.4e-83;
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orbiaceae; Ricinus
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ACC OCC OCC RRY

MEDLINE=91266957; PubMed=2050149

NCBI\_TaxID=3816;
[1]
SEQUENCE FROM N.A.
TISSUE=Leaf;

P28590;

P18590;

Ol-DEC-1992 (Rel. 24, Created)

Ol-DEC-1992 (Rel. 24, Last sequence update)

Ol-DEC-1992 (Rel. 24, Last sequence update)

P1992 (Rel. 24, Last sequence update)

P28-FEB-2003 (Rel. 41, Last annotation update)

Abrin-c precursor [Contains: Abrin-c A chain (rRNA N-glycosidase)

(EC 3.2.2.2); Abrin-c B chain].

Abrus precatorius (Indian licorice) (Crab's eye).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;

eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.

ABRC\_ABRPR

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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                            121 NQEDAEAITHLFTDVQNSFTFAFGGNYDRLEQL-GGLRENIELGTGPL 167
                                                                                                                                                                 61
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                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                     NQEDAEAITHLETDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPL 179
                                                                                                                                                                                DVRHEIPVLPNRVGLPINORFILVELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPD
                                                                                                                                                                                                                                                     MYAVATWLCFGSTSGWSFTLEDNNIFPKQYPIINFTTADATVESYTNFIRAVRSHLTTGA
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                                                                                                                                                            DVRHEIPVLPNRVGLPISORFILVELSNHAELSVTLALDVTNAYVVGCRAGNSAYFFHPD
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N-LINKED (GLCNAC. ..).
N-LINKED (GLCNAC. ..).
F - T (IN REF. 2).
N - D (IN REF. 2).
R -> G (IN REF. 2).
R -> T (IN REF. 2).
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Pred. No. 1.2e-70;
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BY SIMILARITY
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RICIN B-TYPE LECTIN
RICIN B-TYPE LECTIN
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                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                     564;
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QУ
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LEUR. J. Biochem. 198:723-732(1991).
C. -!- FROCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 28 S RRNA. THE CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT PACELLITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT PRECEDES ENDOCYTOSIS.
C. -!- CATALYTIC ACTIVITY: Endobydrolysis of the N-glycosidic bond at one specific adenosine on the 28s rRNA.
C. -!- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
C. -!- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
C. -!- SUBUNIT: DISULFIDE-LINKED DIMER OF A BETA, GAMMA).
C. -!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-
INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
C. -!- SIMILARITY: Contains 2 ricin B-type lectin domains.
                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions we modified and this statement is not removed. Usage by and commodified and this statement is not removed. Usage by and commodified and this statement is not removed. Usage by and commodified and this statement is not removed. Usage by and commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                     ACT_SITE DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X55667; CAA39202.1; -.
                                                                                                                                                                     SEQUENCE
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REPEAT
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Pfam; PF00161; RIP; 1.
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                                                                                                                                                                                        CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plant defense;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000772; Ricin_B_lectin
InterPro; IPR001574; RIP.
                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   K.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S16022; S16022.
75 HEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQE 134
                                    10
                                                                   19
                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PS50231; RICIN_B_LECTIN; 2.
PS00275; SHIGA_RICIN; 1.
fense; Hydrolase; Protein synthesis inhibitor;
                                    LCLAWTCSFSALRCAARTYPPVATNQDQVIKFTTEGATSQSYKQFIEALRQRLTGG--LI 67
                                                                  LCFGSTSGWSFTLEDNNIFP----KQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVR 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lord J.M.,
                                                                                                                                                                                                                                                                                                                                                                      360
403
448
487
529
                                                                                                    Conservative
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                                                                                                                           30.1%;
                                                                                                                                                                       62817 MW;
                                                                                                                    44.18;
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                                                                                                    18;
                                                                                                                                                                                                                                                                     BY SIMILARITY.
INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                    Score 285; DB 1;
Pred. No. 8.6e-20;
                                                                                                                                                                                   PYRROLIDONE CARBOXYLIC ACID
(BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTI
N-LINKED (GLCNAC. . . ) (POTI
N-LINKED (GLCNAC. . . ) (POTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LINKER PEPTIDE (BY SIMILARITY).
ABRIN C B CHAIN (BY SIMILARITY)
RICIN B-TYPE LECTIN 1.
RICIN B-TYPE LECTIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                           2-ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABRIN C A CHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                          2-GAMMA
                                                                                                                                                                                                                                                                                                                                                                                           2-BETA
                                                                                                                                                                                                                                                                                                                                                                                                                          1-GAMMA.
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                                                                                                                                                                     1FD0ABC7D7BA6278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY.
                                                                                                    Mismatches
                                                                                                      62;
                                                                                                                                    Length 562;
                                                                                                                                                                        CRC64;
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                                                                                                                                                                                                                         (POTENTIAL)
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                                                                                                                                                                                        (POTENTIAL)
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                                                                                                      10;
                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kinura M., Sumizawa T., Funatsu G.;

with complete amino acid sequences of the B-chains of abrin-a and abrin-b, toxic proteins from the seeds of Abrus precatorius.";

Biosci. Biotechnol. Biochem. 57:166-169(1993).

-i- FUNCTION: THE A CHAIN IS REPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RRNA.

ABRIN-A IS MORE TOXIC THAN RICIN.

-i- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT PRECEDES ENDOCYTOSIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q06077; P81374;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Abrin-b precursor [Contains: Abrin-b A chain (rRNA N-glycosidase)
(EC 3.2.2.22); Abrin-b B chain].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.

MEDILINE=93132798; PubMed=8421313;

Hung C.-H., Lee M.-C., Lee T.C., Lin J.-Y.;

"Primary structure of three distinct isoabrins determined by cDNA sequencing. Conservation and significance.";

J. Mol. Biol. 229:263-267(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Abrus precatorius (Indian licorice) (Crab's eye).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
               PRINTS; PR00396; SHIGARICIN.
SMART; SM00458; RICIN; 2.
PROSITE; PS50231; RICIN_B_LECTIN; 2.
PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaborate between the Swiss Institute of Bioinformatics and the EMBL outstative European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commendative and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                              -I- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
-I- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
-I- SIMILARITY: Contains 2 ricin B-type lectin domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S TRNA.
-!- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93169023; PubMed=7763422;
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                                                                                                  Pfam; PF00652; Ricin_B_lectin;
Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                     PIR; S32430; S32430.
                                                                                                                                                                                                                             EMBL; M98345; AAA32625.1; -.
                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
                                                                                                                                           InterPro; IPR000772; InterPro; IPR001574;
                                                                                                                                                                                    HSSP; P11140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               125 PASASTYLFPGTQ-RYSLRFDGSYGDLERWAHQTREEISLG 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     135 DAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELG 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                               RIP
                                                                                                                                                                 Ricin_B_lectin.
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RESULT 5
RIPT_TRIKI
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Best Local
                                                                       RIPT_TRIKI STANDARD; PRT; 289 AA. P09989; 01-MAR-1989 (Rel. 10, Created) 01-NOV-1990 (Rel. 16, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) 15-SEP-2003 (Rel. 42, Last annotation update) Ribosome-inactivating protein alpha-trichosanthin precursor (IRNA N-91)cosidase) (EC 3.2.2.2) (Alpha-TCS).
                                         Trichosanthes kirilowii (Mongolian snake-gourd).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledosanthe
eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthe
STRAIN-Maximowicz,
          SEQUENCE FROM N.A.
                                NCBI_TaxID=3677;
                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACT_SITE DISULFID
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REPEAT
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                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                  115 DLERLARQTRQQIPLG
                                                                                                                                                                                                                       160 RLEQLAGNLRENIELG 175
                                                                                                                                                                                                                                                          100 HAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYD 159
                                                                                                                                                                                                                                               59
                                                                                                                                                                                                                                                                                                           40
                                                                                                                                                                                                                                                                                                                                65;
                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                       SDTESIEAGIDVSNAYVVAYRAGNRSYFL---RDAPTSASRYLFTGTQ-QYSLRFNGSYI 114
                                                                                                                                                                                                                                                                                QDQVIKFTTEGATSQSYKQFIEALRQRLTGG--LIHGIPVLPDPTTLQERNRYISVELSN
                                                                                                                                                                                                                                                                                                    QYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSN
                                      Cucurbitales;
                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251
261
272
402
282
325
325
368
413
452
494
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360
400
282
291
291
350
378
426
428
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                                                                                                                                                                                                                                                                                                                                       28.4%;
                                                                                                                                                                                                                                                                                                                                                                      59114 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pyrrolidone carboxylic acid.
                                       Cucurbitaceae;
                                                                                                                                                                                                                                                                                                                              15;
                                                                                                                                                                                                                                                                                                                                                                             AE -> PO (IN REF 2).

S -> N (IN REF 2).

L -> M (IN REF 2).

Y -> D (IN REF 2).

Y -> D (IN REF 2).

N -> S (IN REF 2).

H -> Y (IN REF 2).

H -> W (IN REF 2).

H -> W (IN REF 2).
                                                                                                                                                                                                                                                                                                                                     Score 269; DB 1;
Pred. No. 2.7e-18;
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2-ALPHA.
2-BETA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N ->
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BY SIMILARITY.
PYRROLIDONE CARBOXYLIC ACID (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BY SIMILARITY.
BY SIMILARITY.
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RICIN B-TYPE LECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LINKER PEPTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ' '
z D
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                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D (IN REF. 2).
N (IN REF. 2).
PO (IN REF. 2).
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                                   Trichosanthes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY).
                                                                                                                                                                                                                                                                                                                             50;
                                              core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                               Length 527;
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                                                         Tracheophyta;
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                                                                                                                                                                                                                                                                                                                           6;
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PDB; 1J4G; 28-JAN-03.
PDB; 1NLI; 21-JAN-03.
PDB; 10D2; 24-APR-00.
InterPro; IPR001574; RIP.
Pfam; PF00161; RIP; 1.
PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                            PIR; JT0566; RLTZT.
PDB; 1MRJ; 07-FEB-9;
PDB; 1MRK; 07-FEB-9;
PDB; 1TCS; 10-JUL-9;
PDB; 1J4G; 28-JAN-0;
                                                                                                                                                                                                                                                                                                                                                                             "Studies on crystal structures, active-centre geometry and depurinating mechanism of two ribosome-inactivating proteins."; Biochem. J. 309:285-298(1995).

-i- FUNCTION: TRICHOSANTHIN IS AN ABORTION-INDUCING PROTEIN. IT IS CAPABLE OF INHIBITING HIV-1 INFECTION AND REPLICATION. IT INACTIVATES EUKARYOTIC GOS RIBOSOMAL SUBUNITS.

-i- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28s rRNA.

-i- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
Plant defense;
                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                            entities
                                                                                                                                                                                                                                                                        use by non-profit institumodified and this statement
                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-Maximowicz; TISSUE-Leaf;
MEDLINE-90256790; PubMed-2341400;
Chow T., Feldman R.A., Lovett M., Piatak M.;
"Isolation and DNA sequence of a gene encoding
type I ribosome-inactivating protein.";
J. Biol. Chem. 265:8670-8674(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94344957; PubMed=8066085;
Zhou F., Fu Z., Chen M., Lin Y., Pan K.;
"Structure of trichosanthin at 1.88-A resolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Collins E.J., Robertus J.D., Lopresti M., Stone K.L., Williams K.I Wu P., Hwang K., Piatak M.; "Primary amino acid sequence of alpha-trichosanthin and molecular models for abrin A-chain and alpha-trichosanthin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95344383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang Y., Qian R.Q., Gu Z.W., Jin S.W., Zhang L.Q., Xia Z.X., Tian G.Y., Ni C.Z.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Maximowicz; TISSUE=Tuberous root; MEDLINE=90256789; PubMed=2341399;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        roteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      application."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Scientific evaluation of Tian Hua Fen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Tuberous root;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 24-270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 24-270.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=91153657; PubMed=1999291; Shaw P.C., Yung M.H., Zhu R.H., Ho W.K.K., Ng T.B., Yeung H.W.; "Cloning of trichosanthin cDNA and its expression in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
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                                                                           1MRK;
1TCS;
1J4G;
1NLI;
1QD2;
                                                                                                                                                                                                                                                                                                                                                                           TYPE 1 RIP SUBFAMILY.
                                                                                                                                                                                          M34858; AAA34207.1; -. J05434; AAA34206.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NE=95344383; PubMed=7619070; Wang Y.; Jin S., Wang Y.;
                                                                                                                                                                                                                                                     requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                           07-FEB-95.
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Antiviral; Protein synthesis inhibitor;

Hydrolase;

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            104 SYTLALDYTNAYYVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 162
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82 TISVAIDVTNVYIMGYRAGDTSYFF---
                                     44 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal;
                         25
                                                         Similarity
                         VSFRLSGATSSSYGVFISNLRKALPNERKL-YDIPLL--RSSLPGSQRYALIHLTNYADE
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241 242
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BY SIMILARITY.

IPLL -> LPLI (IN REF. 4).

MISSIG (IN REF. 4).

I -> L (IN REF. 4).

V -> VDACLPRWAVL (IN REF. 4).

KI -> GL (IN REF. 4).

K -> S (IN REF. 4).

Q -> T (IN REF. 2).

MISSING (IN REF. 2).

MISSING (IN REF. 4).

T -> M (IN REF. 2).
                                                   32;
                                                                                                                                                                                                                                                                                                                                                                                                                                 RIBOSOME-INACTIVATING PROTEIN ALPHATRICHOSANTHIN.
MISSING IN MATURE PROTEIN.
                                                         Score 265.5; DB 1
Pred. No. 2.9e-18;
                                                                            5CE09BB630575BB9 CRC64;
                                                   Mismatches
 NEASATEAAKYVFKDAMRKVTLPYSGNYERLQ
                                                                DB 1;
                                                    38;
                                                                Length 289;
                                                    Indels
                                                     7;
                                                     Gaps
   138
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24 INFSLIGATGATYKTFIRNLRTKLTVGTPRVYDIPVLRNAAAGL---ARFQLVTLTNYNG

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RESULT 6
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribosome-inactivating protein bryodin II precursor (rRNA N-
Ribosomes) (EC 3.2.2.22) (BD2).
Bryonia dioica (Red bryony).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Bryonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bioconj, Čhem. 5:423-429(1994).

-I- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS
-I- PROTEIN SYNTHESIS IN ANIMAL CELLS (BY SIMILARITY).

-I- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S IRNA.

specific adenosine on the 28S IRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Siegall C.B., Gawlak S.L., Marquardt H.; "Bryodin 2 a ribosome-inactivating protein isolated from Bryonia dioica.";
                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                        PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
Plant defense; Protein synthesis
                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunoconjugates.";
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                                                                                                                                                                                                                                                          Interpro; IPR001574;
Pfam; PF00161; RIP; ()
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                                                                                                            SEQUENCE
                                                                                                                             CARBOHYD
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67;
                                                              Similarity
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183
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30754 MW; C52BE2F6A873769C CRC64;
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                                                 13;
                                                                Score 261.5; DB 1
Pred. No. 6.8e-18;
                                                                                                                             N-LINKED (GLCNAC.
                                                                                                                                             RIBOSOME-INACTIVATING PROTEIN BRYODIN II. BY SIMILARITY.
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                                                 Mismatches
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15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribosome-inactivating protein karasurin precursor
N-glycosidase) (EC 3.2.2.2).
Trichosanthes kirilowii (Mongolian snake-gourd).
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                                                                                                                                                                                                                                                   EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-97356562; PubMed-9212998;
Mizukami H., Iida K., Kondo T., Ogihara Y.;
"Cloning and bacterial expression of a gene encoding ribosome-inactivating proteins, karasurin-A and karasurin-C, from Trich kirilowii var japonica.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
                                                                                                                                                  PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
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PIR; JU0393; JU0393.
HSSP; P09989; 1MRJ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Root tuber;
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                                                                                                                                      Plant defense; Antiviral;
                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                  between
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              Match
                                                                                                                                                                                                                                                                                                                                                                                                    m. Pharm. Bull. 39:1244-1249(1991).
FUNCTION: ABORTION-INDUCING PROTEIN. IT INACTIVATES EUKARYOTIC 60S RIBOSOMAL SUBUNITS.
CARALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at specific adenosine on the 28S rnna.
SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY
                                                                                                                                                                                                                                                                                                                   s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complete amino acid sequence of an abortifacient protein
                                                                                                                                                                               PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163
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                                                                                                                           Signal.
Similarity
                                                                                                                                                                                                                                                                                          and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                            1 RIP SUBFAMILY
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                                                                                                                                                                                            IPR001574; RIP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PubMed=1914000;
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289
                                          31704 MW;
27.6%;
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                                                                                                                                     Protein synthesis inhibitor;
                                                                                 POTENTIAL.
KARASURIN-C.
KARASURIN-A.
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Pred.
                                                     REMOVED IN MATURE BY SIMILARITY.
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                                       883D3E3242887B26 CRC64;
261.5; DB
No. 7e-18;
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                                                           Tahirov T.H., Lu T.H., Liaw Y.C., Chen Y.-L., Lin J.-Y.;

"Crystal structure of abrin-a at 2.14 A.";

J. Mol. Biol. 250:354-367(1995)

-i- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROT SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBC SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 SABRIN-A IS MORE TOXIC THAN RICIN.

-i- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THA PRECEDES ENDOCYTOSIS.

-i- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic but a company of the company of th
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The complete amino acid sequence of the A-chain of protein from the seeds of Abrus precatorius."; Agric. Biol. Chem. 52:1095-1097(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae: Ahreae. Ahrea
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01-JUL-1989 (Rel. 11, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Abrin-a precursor [Contains: Abrin-a A chain (rRN
(EC 3.2.2.2); Abrin-a B chain].
(EC 3.2.2.2); Abrin-a B chain].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=92371656; PubMed=1505674;
Chen Y.-L., Chow L.-P., Tsugita A
"The complete primary structure of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Evensen G., Mathiesen A., Sundan A.; "Direct molecular cloning and expression
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PROSITE; PS50231; RICIN_B_LECTIN;
PROSITE; PS00275; SHIGA_RICIN; 1.
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PDB; 1ABR; 07-FEB-95.
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InterPro; IPR001574; RIP.
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X54872; -; NOT_ANNOTATED_CDS.
                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase; Protein synthesis inhibitor; Toxin; Repeat; Lectin; 3D-structure; Pyrrolidone carboxylic acid.
ABRIN-A A CHAIN.
    ABRINAM B CHAIN.

RICIN B-TYPE LECTIN 1.

RICIN B-TYPE LECTIN 2.

1-ALPHA.

1-BETA.
1-GAMMA.
2-ALPHA.
2-GAMMIA.
2-GAMMIA.
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Length 528;
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RIP1_BRYDI
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p33185; 095819;
01-0CT-1993 (Rel. 27, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
26-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribosome-inactivating protein bryodin I precu
(EC 3.2.2.22) (BD1).

EC 3.2.2.22) (BD1).

Eukaryota; Viridiplantae; Streptophyta; Embry
Eukaryota; Viridiplantae; Streptophyta; Embry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
                                                                                                             "Characterization of ribosome-inactivating proteins is Bryonia dioica and their utility as carcinoma-reactive
                                                                                                                 Bryonia dioica and their utility as
                                                                                                                                        Marquardt H.;
                                                                                                                                               Siegall C.B., Gawlak S.L.,
                                                                                                                                                          SEQUENCE OF 24-43
                                                                                                                                                                                                                             MEDLINE-89326691; PubMed-2753596;
Montecucchi P.C., Lazzarini A.M., Barbieri L., Stirpe F.,
                                                                                                                                                                                                                                                                 SEQUENCE OF 24-66
                                                                                                                                                                                                                                                                                                 "Cloning and expression of a gene encoding bryodin 1 from Bryonia dioica.";
                                                                                                                                                                                                                                                                                                                     Siegall C.
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                   Biochemistry 36:3095-3103(1997)
                                                                                                                                                                                                                                                                                                                                                              recombinant bryodin 1, Bryonia dioica.";
                                                                                                                                                                                                                                                                                                                                                                                                   Gawlak S.L., Neubauer M., Klei H.E.,
                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97228081; PubMed=9115985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryoph; Spermatophyta; Magnoliophyta; eudicotyledons; co; seurosids I; Cucurbitales; Cucurbitaceae; Bryonia
                                                                                                      immunoconjugates.";
                                                                                                                                                                                                 "N-terminal sequence of some ribosome-inactivating proteins."; Int. J. Pept. Protein Res. 33:263-267(1989).
                                                                                                                                                                                                                                                                                    Patent number US5541110, 30-JUL-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Leaf
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3652;
                                                                                                                                                                                                                                                                                                                                                                                 Molecular, biological,
   PRODUCE A SHORTER PROTEIN.

BIOTECHNOLOGY: Especially useful as immunotoxin toxic
                                     PROTEIN SYNTHESIS IN ANIMAL CELLS.

CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.

PTM: APPEARS TO UNDERGO PROTEOLYTIC CLEAVAGE IN THE C-TERMINAL TO
                                                                                FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               162
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                                                                                                                                                                                                                                                                                                                                                                                             C.B.;
  but
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVTLALDVTNAYVVGYRAGNSAYFFH---PDNQEDAEAITHLFTDVQNRYTFAFGGNYDRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFTTAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL
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is potent once inside target cells.
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                                                                                                                                                                                                                                                                                                                                                                        מ
                                                                                                                                                                                                                                                                                                                                                                  and preliminary structural analysis of
                                                                                                                                             Chace D., Wolff E.A., Mixan B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 5.6e-16;
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                                                                                                                                                                                                                                                                                                                                                                                                   Chang C.Y.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
I precursor (rRNA N-glycosidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Embryophyta;
                                                                                                                        proteins isolated
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        toxicity
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                    for
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                                                                                  INHIBITS
         in rats and
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PROSITE; PS00275; SHIGA_RICIN; 1.

Plant defense; Protein synthesis inhibitor; Hydrolase; Plant defense; Protein synthesis inhibitor; Hydrolase; Plant defense; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                           STRAND
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InterPro; IPR001574; F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 1 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S16491;
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                           31788 MW;
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N-LINKED (GLCNAC. . .)
E->K: REDUCES ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIBOSOME-INACTIVATING PROTEIN BRYODIN I. MISSING IN MATURE PROTEIN. BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RSSIS -> LRHXI (IN REF.
      E966CD9C031A42DB CRC64;
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RESULT 10
NIGB_SAMNI
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Query Match
Best Local S
Matches 59
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P33183; P33184; P93542;

01-OCT-1993 (Rel. 27, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Nigrin b precursor (Agglutinin V) (SNAV) [Contains: Nigrin b A chain (IRNA N-glycosidase) (EC 3.2.2.2); Nigrin b B chain].

Sambucus nigra (European elder).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.
                                 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Girbes T., Citores L., Ferreras J.M., Rojo M.A., Iglesias R., Munoz R., Arias F.J., Calonge M., Garcia J.R., Mendez E.; Munoz R., arias F.J., Calonge M., Garcia J.R., Mendez E.; "Isolation and partial characterization of nigrin b, a non-toxic novel type 2 ribosome-inactivating protein from the bark of Sambucus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Van Damme E.J., Barre A., Rouge P., Van Leuven F., Peumans W.J.; "Characterization and molecular cloning of Sambucus nigra agglutinin V (nigrin b), a GalNAc-specific type-2 ribosome-inactivating protein
                                                                                                                                                                                                                                                                                 <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant Mol. Biol. 22:1181-1186(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94003077; PubMed=8400135;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4202;
                  send
                                                                                                                                                                          SPECIFIC ADENOSINE ON THE 28S TRNA.
SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO TI
INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
SIMILARITY: Contains 2 ricin B-type lectin domains.
                                                                                                                                                                                                                                                                                                                     FUNCTION: NON-TOXIC TYPE 2 RIP WHICH STRONGLY INHIBITS MAMMALIAN PROTEIN SYNTHESIS BUT DOES NOT AFFECT PLANT NOR BACTERIAL PROTEIN SYNTHESIS. THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S. RRNA. THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF NIGRIN B TO THE CELL MEMBRANE THAT PRECEDES
                                                                                                                                                                                                                                                                                 ENDOCYTOSIS.

CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the bark of elderberry (Sambucus nigra)."; J. Biochem. 237:505-513(1996).
                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration
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                  an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F---NEASATEAAKFVFKDAKKKVTLPYSGNYERLQTAAGKIRENIPLG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVLWLLILTIFL-----KSPTVEGD------VSFRLSGATTTSYGVFIKNLREAL
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                                                                                                                 the Swiss Institute of Bioinformatics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 240.5; DB 1
Pred. No. 7.4e-16;
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                                                                                                                 and the
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                                                                                                                       EMBL outstation
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                                                                                                                                                                                                      RESULT 11
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Best Local
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Pfam; PF00652; Ricin_
Pfam; PF00161; RIP; 1
TISSUE-Seed;
TISSUE-Seed;
MEDLINE-91248488; PubMed-1368666;
MEDLINE-91248488; PubMed-1368666;
                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
CONFLICT
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00275; SHIGA_RICIN; 1. PROSITE; PS50231; RICIN_B_LECTIN; Plant defense; Hydrolase; Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00396; SHIGARIO SMART; SM00458; RICIN; 2
                                                                                                                                                                       RIPB_LUFCY P22851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S37382; S37382.
InterPro; IPR000772;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U41299; AAB39475.1;
                                                                                           Luffa cylindrica (Smooth loofah)
Eukaryota; Viridiplantae; Strepto
                                                                                                                                       01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
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                                                            eurosids I; Cucurbitales; Cucurbitaceae; NCBI_TaxID=3670;
                                                                       Spermatophyta; Magnoliophyta; eudicotyledons; eurosids I; Cucurbitales; Cucurbitaceae; Luff;
                                                                                                                             Ribosome-inactivating
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                         SEQUENCE
                                                                                                                   (EC 3.2.2.22).
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                                                                                                                                                                                                                                                                                                                                             9 VIWMYAVATWLCFGSTSGWSFTLEDNNIFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT
                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                           HPDNQEDAEAI -- THLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPL 179
                                                                                                                                                                                                                                                                                                    TGADVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYRAGNSAYFF
                                                                                                                                                                                                                                                                               TGTYEVNGLPVLRRESEVQVKSRFVLVPLTNYNGNTVTLAVDVTNLYVVAFSGNANSYFF
                                                                                                                                                                                                                                      ----KDATEVQKSNLFVGTKQN-TLSFTGNYDNLETAANTRRESIELGPSPL
                                                                                                                                                                                                                                                                                                                                                                                                              563 AA;
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                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    297
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                                                                                                                                       Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal.
                                                                                                                             protein luffin-B
           Funatsu G.;
                                                                                            Streptophyta;
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BY SIMILARITY.

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BY SIMILARITY.

BY SIMILARITY.

BY GICNAC. . .) (POTEN INTERCHALL (GICNAC. . .) (POTEN INTERCHALL (POTEN INTERCHALL) (POTEN INTERCHALL)
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NIGRIN B B CHAIN.
RICIN B-TYPE LECTIN :
RICIN B-TYPE LECTIN :
                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED
                                                                                                                                                                                                                                                                                                                                                                              Score 236; DB 1;
Pred. No. 4.5e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2-ALPHA.
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                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                         (Sponge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    synthesis inhibitor; Toxin; Repeat;
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                                                                                                                                                    update)
                                                                                                                                                                                                                                                                                                                                                                                                                          (IN REF.
                                                                                                                                                                                     250
                                                                                                                                       update)
                                                                                                                               (rRNA N-glycosidase)
                                                                                             Embryophyta; Tracheophyta;
                                                                                                                                                                                     ₹
                                                                                                                                                                                                                                                                                                                                                                      65;
                                                                                      core
                                                                                                                                                                                                                                                                                                                                                                                       Length 563;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL).
(POTENTIAL).
                                                                                    eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                      20;
                                                                                      Rosidae;
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                                                       T "Complete mino acid sequence of the A chain of mistletoe lectin I.";

L FEBS Lett. 399:153-157(1996).

C --- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYPWHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S. RRNA. THE B CHAIN BINDS TO CELL RECEPTORS AND PROBABLY FACILITATES THE ENTRY C. INTO THE CELL OF THE A CHAIN, B CHAINS ARE ALSO RESPONSIBLE FOR C. CELL AGGLUTINATION (LECTIVA ACTIVITY).

C --- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28s rrna.

C --- SUBUNIT: Disulfide-linked dimer of A and B chains.

C --- SUBUNIT- Disulfide-linked dimer of A subunity and subunity and the studied in clinical trials in cancer patients as it may slow the growth of cancer cells and be an effective treatment for solid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Beta-galactoside specific lectin I A chain (MLA) (ML-I A) (TRNA N-91ycosidase) (EC 3.2.2.22)
Yiscum album (European mistletoe).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MLA_VISAL
P81446;
                                                                                                                                                                                                                                                                                                                                   STRAIN-Subsp. album;
MEDLINE-97134581; PubMed-8980141;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                     Soler M.H., Stoeva S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Toxin.
ACT_SI
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HSSP; P16094; 1AHC.
InterPro; IPR001574; RIP.
Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                           Voelter W.
                                                                                                                                                                                                                                                                                                                                                                                                                            Santalales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00396; SHIGARICIN PROSITE; PS00275; SHIGA_RIC1
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28s rrna.
-i- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Complete amino acid sequence of luffin-b, a ribosome-inactivating protein from sponge gourd (Luffa cylindrica) seeds.";
Agric. Biol. Chem. 55:229-238(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
     AND NON-GLYCOSYLATED SIMILARITY: BELONGS T
                                 MISCELLANEOUS: TWO ISOFORMS OF MLA EXIST:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            117 AAGKIREKIPLG 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          164 LAGNLRENIELG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60 AITMAIDVTNVYIMGYLVNSTSYF---ANESDAKLASQYVFKGSTLVTIPYSGNYERLQN 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 INFTTAGATYQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 103
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250 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                         Santalaceae;
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     BELONGS TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 I
27293 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.0%;
                                                                                                                                                                                                                                                                                                              Schwamborn C., Wilhelm S., Stiefel T.,
                    FORM MLA
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THE RIBOSOME-INACTIVATING PROTEIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31;
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Pred. No. 9e-14;
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; F01A8DC8A1078700 CRC64;
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                                  GLYCOSYLATED FORM MLA
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Best Local
                                                                                                                                                                                                           P29339;
P29339;
P1992 (Rel. 24, Created)
Ol-DEC-1992 (Rel. 24, Last sequence update)
P1-SEP-2003 (Rel. 42, Last annotation update)
P1-SEP-2003 (Rel. 42, Last annotation update)
P1-SEP-2003 (Rel. 42, Last annotation II precursor (rRNA Ribosome-inactivating protein momordin II precursor (rRNA N-91)cosidase) (EC 3.2.2.2)
Momordica balsamina (Bitter gourd) (Balsam pear).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Traci Spermatophyta; Magnoliophyta; eudicotyledons; core eudicoideurosids I; Cucurbitales; Cucurbitaceae; Momordica.
                                                                                                 Ortigao M., Better M.;
"Momordin II, a ribosome inactivating protein from Momordica balsamina, is homologous to other plant proteins.";
This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                   Nucleic Acids Res. 20:4662-4662(1992).
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
                                                                                                                                                     MEDLINE=93027170; PubMed=1408771;
                                                                                                                                                                   TISSUE=Seed
                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                              RIP2_MOMBA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant defense;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00161; RIP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; P11140; 1ABR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /ARIANT
                                           SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 1 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE 2 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PD0018; PD0018
                                                                                                                                                                                                                                                                                                                                                                                                                                                          166 GNLRENIELG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 TLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48 TAGATYQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPIN--QRFILVELSNHAELSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9 THOTTGEEYFREITLLRDYVSSGS-FSNEIPLL-RQSTIPVSDAQRFVLVELTNQGQDSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               GH-RDQIPLG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAAIDVTNAYVVAYQAGDQSYFLR-DAPRGAE--THLFTGT-TRSSLPFNGSYPDLERYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase; Toxin;
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1116
1134
140
140
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179
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1190
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2218
231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22.8%;
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V -> I (IN MLA').

N -> T (IN MLA').

P -> T (IN MLA').

DQ -> EE (IN MLA').

T -> S (IN MLA').

T -> S (IN MLA').

T -> A (IN MLA').

T -> B (IN MLA').

Y -> D (IN MLA').

Y -> B (IN MLA').

Y -> M (IN MLA').

PP -> ST (IN MLA').
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 216.5; DB 1;
Pred. No. 1.3e-13;
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D -> S (IN MLA').
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                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                             286
                                                                                                                                                                                                                                             Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Glycoprotein; Lectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40;
                                                                                                                                                                                                                                  core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 254;
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            a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9;
                                                                                                                                                                                                                                  Rosidae;
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EMBL outstation

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RESULT 14
RIP1_CUCFI
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                               SEQUENCE FROM N.A.

Yamada T., Ohki S.T., Osaki T.;

"Cloning and analysis of a cDNA coding a putative ribosome-
inactivating protein from Cucumis figarei.";

Plant Biotechnol. 17:337-340(2000).

-1-CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one
specific adenosine on the 28s TRNA.

- PROTECT ACTIVITY: ENDOHYDROW TRNA.

- PROTECT ACTIVITY: TO THE PROCESS TRNA.

- PROTECT ACTIVITY: TO THE PROCESS TRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00396; SHIGARICIN. PROSITE; PS00275; SHIGA_RICI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00161; RIP; 1
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                                                                         use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities
                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Putative ribosome-inactivating protein precur
                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restrained to the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3D-structure.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Cucumis figarei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RIP1_CUCFI
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                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=131071;
                                                                                                                                                                                                                                                                                                                                                                                                                                        (EC 3.2.2.22)
                                                                                                                                                                                     TYPE 1 RIP SUBFAMILY.
                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1CF5; 07-JUN-99.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      104
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 103
 P16094;
                 AB045560; BAB19677.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYTLALDYTNAYYVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQ 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LAGNLRENIELG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISVAIDVTNYYVVAYRTRDVSYFF---KESPPEAYNILFKGTR-KITLPYTGNYENLQT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VNFDLSTATAKTYTKFIEDFRATLPFSHKV-YDIPLLYSTIS--DSRRFILLDLTSYAYE 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181
286 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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24
   IAHC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32031 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 210.5;
Pred. No. 5.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          286 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       precursor (rRNA N-glycosidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6e-13;
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                                                                                  Usage by and
                                                                                                                                  and the EMBL outstation
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                                                                                                                   restrictions
                                                                                                       S,
                                                                                                                                                      a collaboration
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                   Gelonium multiflorum (Euphorbiaceae himalaya).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids I, Malpighiales; Euphorbiaceae; Gelonium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-OCT-1993 (Rel. 27, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribosome inactivating protein gelonin precursor (rRNA N-glycosidase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIPG_
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                                                  "X-ray structure of gelonin at 1.8-A resolution.";
J. Mol. Biol. 250:368-380(1995).
-i- CATALTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at
            specific adenosine on the 28S rRNA.
-!- SUBUNIT: Homodimer.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY
                                                                                                                                                                                                                                                                        inactivating protein from Gelonium multiflorum.
Gene 134:223-227(1993).
                                                                                                                                                                                                                                                                                                    Nolan P.A., Garrison D.A., Better M.; "Cloning and expression of a gene encoding gelonin, a ribosome-
                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=3979
                                                                                               Kannan K.K.;
                                                                                                                        X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
MEDLINE=95333189; PubMed=7608981;
                                                                                                                                                                                                           Montecucchi P.C.,
                                                                                                                                                                                                                        MEDLINE-89326691;
                                                                                                                                                                                                                                      TISSUE=Seed
                                                                                                                                                                                                                                                   SEQUENCE OF 47-93.
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=94085781; PubMed=7916721;
                                                                                                          Hosur M.V., Nair B., Satyamurthy P., Misquith S., Surolia
                                                                                                                                                                               "N-terminal sequence of some ribosome-inactivating
                                                                                                                                                                                            Lappı U.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        EC 3.2.2.22).
                                                                                                                                                                 Int. J.
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TYPE 1 RIP SUBFAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       103 LSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLE
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103
110
252
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                                                                                                                                                                  Protein
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                                                                                                                                                                                                                         PubMed=2753596;
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286 F
185 F
103 N
110 N
252 N
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                                                                                                                                                                  Res.
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                                                                                                                                                                     33:263-267(1989).
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N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
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ACT_SITE
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PROSITE; PS00275; SHIGA_RICIN; FALSE_NEG.
Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; L12243; AAA16312.1; -. PIR; JT0753; JT0753. HSSP; P09989; 1MRJ.
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SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                    PROPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                    171 TIDLGIEPL 179
                             171 NIELGNGPL 179
                                                                             116 VVGYRAGNSAYFFH--PDNQEDAEAITHLFTD-VQNRYTFAFGGNYDRLEQLAGN--LRE 170
                                                                                                            63 YVNFLNELRYKLKPEGN-SHGIPLLRKKCDDP-GKCFVLVALSNDNGQLAEIAIDVTSVY 120
                                                                                                                                        56 YTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAY 115
                                                                                                                                                                     3 GNMKVYWIKIAVATWFCCTTIVLGSTARIFSLPTNDEEETSKTLGLDTVSFSTKGATYIT 62
                                                                                                                                                                                                 5 GNTIVIWM-YAVATWLC-----FGSTSG-WSFTLEDNNIFPKQYPI--INFTTAGATVQS 55
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93 P -> D (IN REF. 2).
35418 MW; 1252F3E710901B85 CRC64;
                                                                                                                                                                                                                                21.9%; Score 208; DB 1; Length 316; 36.5%; Pred. No. 1.1e-12; itive 26; Mismatches 68; Indels ?
                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. . .).
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Search completed: September 16, 2003, 11:46:02 Job time: 7.2752 secs

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Result
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Q014BW3
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Q94bw4 cinnamomum
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Q38760 abrus preca
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Q38761 abrus preca
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0 abrus preca
4 trichosanth
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	P93543	041358	022415	004357	Q9M653	Q8RXH7	Q8W243	Q8LKQ6	Q8GZP0	004356	Q8RXH6	Q8LKQ5	Q9FUV7	Q41257	004072	Q9FSH2	004358	Q8LKQ4	Q8GZN9	004071	Q9M654	Q8VYU0	086000	Q8GT32	Q945S2	Q8S452	Q41611	Q38761	Q96236
	P9354	0413	02241	00435	29m65	Q8rxh7	Q8w243	Q81kc	12580	00435	08rxh6	081ka	Q9fuv	041257	00407	Q9fsl	004358	081k	Q8gz1	0040	09m654	08vγ	0009	Q8qt32	0945	0854	Q4161:	0387	Q962
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## ALIGNMENTS

RESULT 1 Q41174

041174

NON\_TER SEQUENCE PRINTS; PR00396; SHIGARICIN.
SMART; SM00458; RICIN; 2.
PROSITE; PS50231; RICIN, BLIECTIN; 2.
PROSITE; PS00275; SHIGA\_RICIN; 1.
PROSITE; PS00338; SOMATOTROPIN\_2; 1. -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

EMBL; \$40366; AAB22582.1; -.

HSSP; P02879; IBB6.

InterPro; IPR000772; Ricin\_B\_lectin.

InterPro; IPR001574; RIP.

InterPro; IPR001574; RIP.

InterPro; IPR001400; Somatotropin.

Pfam; PF00652; Ricin\_B\_lectin; 6.

Pfam; PF00151; RIP; 1. Roberts L.M., Tregear J.W., Lord J.M.;
"Molecular cloning of ricin.";
"Molecular cloning of ricin.";
Targeted Diagn. Ther. 7:81-97(1992).
-1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 28S RRNA. Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids I; Malpighiales; Euphorbiaceae; Ricinus. 01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Proricin A chain (EC 3.2.2.22) (rRNA N-glycosidase) Hydrolase; Toxin. MEDLINE=92338377; PubMed-1633311; SEQUENCE FROM N.A. NCBI\_TaxID=3988; Ricinus communis (Castor bean). 541 AA; PRELIMINARY; 60281 MW; PRT; 2B7B2CDEF1F2E9D9 CRC64; 541 À core eudicots; Rosidae;

Q9avr2 Q81pv7 Q9m6e9 Q96235

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RESULT 2
Q94BW3
ID Q94B
AC Q94B
AC Q94B
DT Q1-I
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Type 2 ribosome inactivating protein cinnamomin III precursor
(EC 3.2.2.2) (TRNA N-glycosidase).
Cinnamomum camphora (Camphor tree).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheoph
Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL; AY039803; AAK82460.1; -.
Interpro; IPR000772; Ricin_B_lectin.
Interpro; IPR001574; RIP.
Pfam; PF00652; Ricin_B_lectin; 6.
Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00396; SHIGARICIN. SMART; SM00458; RICIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-2001) to the EMBL/GenBank/DDBJ-i- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genes encoding cinnamomin proteins and study of their expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gong Z.Z., Liu W.Y.;
ar cloning of three type 2 RIP (ribosome-inactivating protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GNYDRLEQLAGNLRENIELGNGPL 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GNYDRLEQLAGNLRENIELGNGPL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHDIPVLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PS50231; RICIN_B_LECTIN; 2.
                                                                                                                                                                                                RLEQLAGNLRENIELGNGPL 179
                                                                                                                                                                                                                                                         AADSPVTLAVDVTNAYVVAYRTGSQSFFLREDNPD--PAIENLLPDTK-RYTFPFSGSYT 148
                                                                                                                                                                                                                                                                                                                                                                                                                  YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSN- 99
                                                                                                                                                                                                                                                                                                                                                                  YQTVTFTTKNATKTSYTQFIEALRAQLASGEE-PHGIPVMRERSTVPDSKRFILVELSNW 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                580 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78.6%;
99.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64421 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 745; DB 10;
Pred. No. 2.1e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 308.5; DB pred. No. 8.5e-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE 2 RIBOSOME-INACTIVATING PROTEIN CINNAMOMIN III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      940D10F01E7FB558 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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Q94BW5;
Q1-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yang Q., Gong Z.Z., Liu W.Y.;
"Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
genes encoding cinnamomin proteins and study of their expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cinnamomum camphora (Camphor tree).
Eukaryota; Viridiplantae; Streptophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Type
(EC 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spermatophyta; Magnoliophyta; Laurales;
                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-OCT-2002 (TrEMBLrel.
          SEQUENCE FROM N.A.

Xie L., Liu W.-Y., Wang E.-D.;

Xie L., Liu W.-Y., Wang E.-D.;

Molecular cloning of cinnamomin A-, B-chain and the expression,

purification, characterization and mutagenesis of the A-Chain.";

pubmitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

-i- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
                                                                                                                                                                         Type II ribosome-inactivating protein cinnamomin (EC 3.2.2.22) (rRNA
                                                                                                                                                                                                                                                Q9FV22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00458; RICIN; 2.
PROSITE; PS50231; RICIN_B_LECTIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00652; Ricin_B_lectin; 5. Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=13429;
                                                                                                                        Spermatophyta; Magnoliophyta;
                                                                                                                         Eukaryota; Viridiplantae; Streptophyta;
Spermatophyta; Magnoliophyta; Laurales;
                                                                                                                                               Cinnamomum camphora (Camphor tree).
                                                                                                                                                                                                                                   Q9FV22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          patterns
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                         NCBI_TaxID=13429;
                                                                                                                                                                -glycosidase) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e 2 ribosome-inactivating protein cinnamomin I precursor 3.2.2.22) (rRNA N-glycosidase).
SPECIFIC ADENOSINE ON THE 28S RRNA
                                                                                                                                                                                                                                                                                                                  149 DLEGVAGERREEILLGMDPL
                                                                                                                                                                                                                                                                                                                                            160 RLEQLAGNLRENIELGNGPL 179
                                                                                                                                                                                                                                                                                                                                                                                               100 HAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYD 159
                                                                                                                                                                                                                                                                                                                                                                                                                             S
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                                                                                                                                                                                                                                                                                                                                                                        92 AADSPYTLAVDVTNAYVVAYRTGSQSFFLREDNPD--PAIENLLPDTK-RYTFPFSGSYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                            YQTVTFTTKNATKTSYTQFIEALRAQLASGEE-PHGIPVMRERSTVPDSKRFILVELSNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       581 AA; 64215 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHIGARICIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32.2%; Score 305.5; 50.7%; Pred. No. 1.
                                                                                                                                                                                          16, Created)16, Last sequence update)22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CINNAMOMIN I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE 2 RIBOSOME-INACTIVATING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6E8F5FB8FBA3D196 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  581
                                                                                                                                                                                                                                                   549 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.6e-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lauraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Embryophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Š
                                                                                                                          Lauraceae;
                                                                                                                                   Embryophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                THE N-GLYCOSIDIC BOND AT ONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                             Cinnamomum
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                                                                                                                                         Tracheophyta;
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RESULT 5
Q948W4
ID Q948W
AC Q948W
DT 01-D
DT 01-D
DT 01-D
DT 01-D
DT 01-W
CC Cint
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OX NCB
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                                        Query Match
Best Local
                              Matches
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                                                                                                                01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Type 2 ribosome-inactivating protein cinnamomin II precursor
(EC 3.2.2.22) (rRNA N-glycosidase).
Cinnamomum camphora (Camphor tree).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
                                                                      SEQUENCE
                                                                                                   Hydrolase; Signal; Toxin.
                                                                                                                                                                                                                                                         genes encoding cinnamomin proteins and study of their expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00396; SHIGARICIN.
SMART; SM00458; RICIN; 2.
PROSITE; PS50231; RICIN_B_LECTIN;
                                                                                                                                                                                                                                                      patterns.";
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                            Q94BW4
                                                                                                                                                                                                                                                                  Yang Q., Gong Z.Z., Liu W.Y.;
"Molecular cloning of three type 2 RIP (ribosome-inactivating protein)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hydrolase; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00652; Ricin_B_lectin; 5.
Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. BMBL; AF259548; AAF68978.2; -. HSSP; P02879; 2AAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
                                      Local
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  41 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 DLEGVAGERREEILLGMDPL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100 HAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYD 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160 RLEQLAGNLRENIELGNGPL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 AADSPVTLAVDVTNAYVVAYRTGSQSFFLREDNPD--PAIENLLPDTK-RYTFPFSGSYT 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 YPIINFTTAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLDNRVGLPINQRFILVELSN- 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 YQTVTFTTKKATKTSYTQFIEALRAQLASGEE-PHGIPVMRERSTVPDSKRFILVELSNW
                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                   580 AA; 64265 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              549 AA;
                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                          ω
                                                                                          580
                                    32.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.0%; Score 303.5; DB 10; Length 549; 50.7%; Pred. No. 2.4e-20; tive 19; Mismatches 45; Indels 5;
                           21;
                                     Score 303.5;
Pred. No. 2.
                                                                                    POTENTIAL.

TYPE 2 RIBOSOME-INACTIVATING PROTEIN
                                                                               CINNAMOMIN II
                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                         Mismatches
                                                                 37E4289ECCE0CBFF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                       580 AA.
                                   .5e-20;
                                            DB 10;
                         44; Indels
                                             Length 580;
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                        Gaps
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  RESULT 7
Q38760
ID Q387
AC Q387
DT 01-N
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Q38760;
01-NOV-1998
01-NOV-1998
                                 Q38760
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Query Match
Best Local Similarity
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SEQUENCE
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Abrund (EC 3.2.2.2) (rRNA N-glycosidase) (Fragment).
Abrus precatorius (Indian licorice) (Crab's eye).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid:
eurosids [; Fabales; Fabaceae; Papillonoideae; Abrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
Pfam; PF00552; Ricin_B_lectin; 6.
Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hung C.-H., Lee M.-C., Lee T.-C., Lin J.-Y.;

"Primary structure of three distinct isoabrins determined by cDNA sequencing: conservation and significance.";

J. Wol. Biol. 229:263-267(1993).

-i- CATALYTIC ACTIVITY: ENDOMYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydrolase; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50231; RICIN_B_LECTIN; 2. PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00396; SHIGARICIN. SMART; SM00458; RICIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. EMBL; M98346; AAA32626.1; -. HSSP; P11140; IABR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93132798; PubMed=8421313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3816;
                                                      160 RLEQLAGNLRENIELG 175
                                                                                                                                                       100 HAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYD 159
                                                                                                                                                                                                                                                40 QYPIINETTAGATVQSYINEIRAVRGRLITGADVRHEIPVLPNRVGLPINQRFILVELSN 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 RLEQLAGNLRENIELGNGPL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 HAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYD 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149 DLERVAGELREEILLGMDPL 168
                                                                                                                                                                                                                                                                                                                                      66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92 AADSPVALAVDVTNAYVVAYRTGSQSFFLREDNPD--PAIENLLPDTK-RYTFPFSGSYT 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ω
W
DLERWAHQTREEISLG 130
                                                                                                       SERESIEVGIDVTNAYVVAYRAGSQSYFL---RDAPASASTYLFPGTQ-RYSLRFDGSYG 114
                                                                                                                                                                                                                 QDQVIKFTTEGATSQSYKQFIEALRQRLTGG---LIHDIPVLPDPTTVEERNRYITVELSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                          528
528 AA;
                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                         528
58870 MW; 62ED42FB8FFE60F8 CRC64;
                                                                                                                                                                                                                                                                                                                        29.7%; Score 282; DB 10; 48.5%; Pred. No. 2.5e-18; tive 16; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        528 AA
                                                                                                                                                                                                                                                                                                                                48;
                                                                                                                                                                                                                                                                                                                                                                           Length 528;
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                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                    58
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(Tremblrel. (Tremblrel. (

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Created)
Last sequence update)

PRT;

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Biol. Chem. 266:6848-6852(1991).

-: FUNCTION: THE A CHAIN IS REPONSIBLE FOR INHIBITING PROTEINTS SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSC SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 SEARIN-A IS MORE TOXIC THAN RICIN.

-: FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FUNCTION: THE BCHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMUL; X54872; CAA38654.1; -. HSSP; P11140; 1ABR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Abrin-E (RRNA N-glycosidase) (EC 3.2.2.22) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <del>-</del>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Direct molecular cloning and expression of two distinct abrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=91201329; PubMed=2016300;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=3816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Abrus precatorius (Indian
                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosic
eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
                                                                                                                              01-DEC-2001 (TrEMBLrel. 01-MAR-2003 (TrEMBLrel.
                                                                                                                                                              Q94KE4;
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase; Glycosidase; Toxin; Repeat; Glycoprotein; Lectin
CHAIN 1 252 ABRIN E, A CHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00161; RIP;
NCBI_TaxID=3677; [1]
                                eurosids
                                                                                Trichosanthes kirilowii (Mongolian snake-gourd)
                                                                                                                Trichosanthin
                                                                                                                                                                                                Q94KE4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIFIC ADENOSINE ON THE 28S RRNA.
SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
SUBUNIT: DISULFIDE-LINKED DIMER OF TWO DOMAINS, EACH DOMAIN
DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN
CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
SIMILARITY: TO OTHER BACTERIAL AND PLANTS RIBOSOME-INACTIVATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRECEDES ENDOCYTOSIS CATALYTIC ACTIVITY: I
                                                                                                                                                                                                                                                                             120
                                                                                                                                                                                                                                                                                                          164 LAGNIRENIELG 175
                                                                                                                                                                                                                                                                                                                                          64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63;
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                                                                                                                                                                                                                                                                                                                                                                        SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQ
                                                                                                                                                                                                                                                                                                                                          SIEVGIDVTNAYVVAYRAGSQSYFL---RDAPASASTYLFTGTQ-RYSLRFDGSYGDLER
                                                                                                                                                                                                                                                                                                                                                                                                                                      INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL
                                                                                                                                                                                                                                                                             WAHQTREQISLG
                                                                                                                                                                                                                                                                                                                                                                                                      IKFSTEGATSQSYKQFIEALRERLRGG--LIHDIPVLRDPTTVEERNRYITVELSNSERE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     252
252 AA;
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                                                                                                                                                              (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                PRELIMINARY;
                                                                                                               precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28309 MW; BBFC846B9E92B5DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28.0%;
                                                                                                                                                                                                                                                                               131
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                                                                                                               19, Created)
19, Last sequence update)
23, Last annotation update)
(EC 3.2.2.22) (rRNA N-glycosidase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 265; DB 10;
Pred. No. 3.9e-17;
                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Crab's eye).
                                                                                                                                                                                                 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10;
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28 S RRNA
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                                                     Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                   Query Match
Best Local S
Matches 57
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Best Local :
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EMBL, AF367252; AAK52960.1; -.
InterPro; IPR001574; RIP.
Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000
01-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                        Phan Van Chi, Nguyen Thuy Ha, Le Tran Binh;
Phan Van Chi, Nguyen Thuy Ha, Le Tran Binh;
"Genomic DNA Clone for mature typ-1 ribosome-inactivating protein from
"Inchosanthes sp. sample 01 Bec Kan 8-98 Vien CNSH (Hanoi).";

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
-!- CATALYTIC ADENOSINE ON THE 28S RRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trichosanthes sp. Bac Kan 8-98. Eukaryota; Viridiplantae; Strep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Trichobakin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase; Signal; Toxin.
                                                                                                                                                                                                                                                              PRINTS; PR00396; SHIGARICIN. PROSITE; PS00275; SHIGA_RICIN;
                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY
                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB039324; BAA92530.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=118182;
                                                                                                                                                                                     NON_TER
                                                                                                                                                                                                             NON_TER
                                                                                                                                                                                                                                        Hydrolase; Toxin.
                                                                                                                                                                                                                                                                                                                    Pfam; PF00161; RIP;
                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                  HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                              Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   139 TAAGKIRENIPLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163 QLAGNLRENIELG 175
                                                                                                                                                                                                                                                                                                                                                                  P09989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   44 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 VSFRLSGATSSSYGVFISNLRKALPNERKL-YDIPLL--RSSLPGSQRYALIHLTNYADE
44 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISVAIDVTNVYIMGYRAGDTSYFF---NEASATEAAKYVFKDSMRKITLPYSGNYERLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                289 AA;
                                                                                                                                                            247
247 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TREMBLrel. 22, Last annotation update)
(EC 3.2.2.22) (rRNA N-glycosidase) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24
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247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42.18;
                                                                                                                                                            27199 MW; 89811AC32892F03F CRC64;
                                                                              27.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32;
                                                           32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRICHOSANTHIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 263.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                   Pred.
                                                                                                            Score 261.5;
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                                                                                      No. 8.1e-17
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                                                                                                              DB 10;
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                                                                Indels
                                                                                                            Length 247;
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                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
       Sambucus nigra (European elder).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.
                                                                                                  Ribosome inactivating protein precursor (EC 3.2.2.22) (rRNA N-glycosidase).
                                                                                                                                         01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                         004367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zheng H., Wang B., Shaw P., Yeung H.;

"[Cloning and DNA sequencing of the gene encoding trichosanthin].";

I Chuan Hsuch Pao 21:42-51(1994).

-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 28S RRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update
Trichosanthin (EC 3.2.2.22) (TRNA N-glycosidase).
TRICHOSANTHIN, TCS.
TRICHOSANTHEN, TCS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; S70176; AAB31048.1; -. HSSP; P09989; IMRJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-94271613; PubMed=8003348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=3677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q41216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10
                                                                                                                                                                                                                                                                                                                                                                                 163 QLAGNLRENIELG 175
                                                                                                                                                                                                                                                                                                                                                       139 TAAGKIRENIPLG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF00161; RIP; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 IAAGKIRENIPLG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163 QLAGNLRENIELG 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25 VSFRLSGATSSSYGVFISNLRKALPNERKL-YDIPLL--RSSLPGSQRYALVHLTNYADE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                TISVAIDVTSVYIMGYRAGDTSYFF---NEASATEAAKYVFKDAMRKVTLPYSGNYERLQ 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISVAIDVTNVYVMGYRAGDTSYFF---NEASATEAAKYVFKDAKRKVTLPYSGNYERLQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYTLALDYTNAYVYGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSFRLSGATSSSYGVFISNLRKALPYERKL-YDIPLL--RSTLPGSQRYALIHLTNYADE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Toxin.
289 AA; 31650 MW;
                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.6%;
42.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 261.5; DB
Pred. No. 1e-16;
                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        286AC14D48BCA175 CRC64;
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                                                                                                                                                                                                                                       563 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       289
                                                     Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 289;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                  Girbes T., Iglesias R., Perez Y., Ferreras J.M., Citores L.,
"Molecular cloning of ebulin 1.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 28S RRNA.
                                            -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. EMBL; AJ400822; CAC33178.1; -. HSSP; P02879; 2AAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Ribosome-inactivating protein precursor (EC 3.2.2.22) (rRNA
                         InterPro;
                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                   Sambucus ebulus
                                                                                                                                                                                                                                                                                                                                                                                                                           N-glycosidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9AVR2;
                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                          NCBI_TaxID=28503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9AVR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The major elderberry (Sambucus nigra) fruit protein is a lectin derived from a truncated type 2 ribosome-inactivating protein."; plant J. 12:1251-1260(1997).
-i- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50231; RICIN_B_LECTIN; 2. PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00396; SHIGARICIN. SMART; SM00458; RICIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
Pfam; PF00652; Ricin_B_lectin; 6.
Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                         ISSUE=Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase; Signal; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U76524; AAC15886.1; HSSP; P02879; 2AAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peumans W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Van Damme E.J., Roy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 HPDNQEDAEAI -- THLFTDVQNRYTFAFGGNYDRLEQLAGNLRENIELGNGPL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----KDATQLQKSNLFVGTR-QHTLPFTGNYDNLETAAGTRRESIELGPSPL 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGADVRHEIPVLPNRVGLPINQRFILVELSNHAELSVTLALDVTNAYVVGYRAGNSAYFF 128
IPR000772; Ricin_B_lectin
IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGTYEVNGLPVLRRESEVQVKNRFVLVLLTNYNGNTVTLAVDVTNLYVVAFSANANSYFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MLYLYIVVLAICSVGIQG---
                                                                                                                                                                                                                                                                                                             campanulids; Dipsacales; Adoxaceae; Sambucus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               563 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62336 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.7%;
35.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 253; DB 10;
Pred. No. 1.6e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
RIBOSOME INACTIVATING PROTEIN,
RIBOSOME INACTIVATING PROTEIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3ED2B6C08E796205 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rouge P., Van Leuven F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----IDYPSVSFNLAGAKSATYRDFLKNLRTIVA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         564 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 10;
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CHAIN.

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QBLPV7
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Best Local
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Best Local
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PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00396; SHIGAL SMART; SM00458; RICIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U1-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2003 (TrEMBLrel. 23, Trichosanthin precursor (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

Yuan H., Wang Y., Liu T., An C., Chen Z.;

Yuan H., Wang L., Wang Y., Liu T., An C., Chen Z.;

"Trichosanthes kirilowii trichosanthin precursor (TCS) gene.";

Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.

-I- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
-I- CATALYTIC ADENOSINE ON THE 28S RRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8LPV7;
01-OCT-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q8LPV7
                                                                                                                                                                                                                                                                                                                                                                                                                              pfam; pF00161; RIP; 1.
pRINTS; pR00396; SHIGARICIN.
pROSITE; pS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING EMBL; AY082348; AAM22782.1; -. InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Trichosanthes kirilowii (Mongolian snake-gourd)
                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                         Hydrolase; Signal; Toxin.
SIGNAL 1 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Fragment).
                                                                                                                                                                                                                                                                                                                      NON_TER
                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=3677;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 AELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAI--THLFTDVQNRYTFAFGGNY 158
                104 SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28
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                                                                      25 VSFRLSGATSSSYGVFISNLRKALPYEKKL-YDIPLL--RSSLSGSQRYALIYLTNYADE
                                                                                                                                                                                       55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNLETAAGTRRESIELGPNPL 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DRLEQLAGNLRENIELGNGPL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NGDTVTSAVDVTNLYLVAFSANGNSYFF-----KDATELQKSNLFLGT-TQHTLSFTGNY
                                                                                                                         INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   564 AA;
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                                                                                                                                                                                                                                                                                             270 AA;
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                                                                                                                                                                                                                                                                                                                         270
                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                               29683 MW;
                                                                                                                                                                                                              26.3%; Score 249.5;
41.4%; Pred. No. 1.3
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Last annotation update)
3.2.2.22) (rRNA N-glycosidase)
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EBULIN L A-CHAIN.
EBULIN L B-CHAIN.
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                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                  TRICHOSANTHIN.
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                                                                                                                                                                                                                                                                                                  531713B754F9B769 CRC64;
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                                                                                                                                                                                       Mismatches
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<del>..</del>
                                                                                                                                                                                                                   1.3e-15
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                                                                                                                                                                                                                                          DB_10; Length 270;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
preproagglutinin (EC 3.2.2.22) (rRNA N-glycosidase).
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                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00396; SHIGARICIN.
SMART; SM00458; RICIN; 2.
PROSITE; PS50231; RICIN B_LECTIN;
PROSITE; PS50275; SHIGA_RICIN; 1.
Hydrolase; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Abrus precatorius (Indian licorice) (Crab's eye).
Eukaryota; viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9M6E9;
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Pfam; PF00161; RIP; 1
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                                         01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P11140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lin J.Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20102702; PubMed=10636890;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=3816;
                            Abrin A chain E164A/R167L (EC 3.2.2.22) (rRNA N-glycosidase)
Abrus precatorius (Indian licorice) (Crab's eye)
                                                                                        Q96235;
                                                                                                    Q96235
                (Fragment)
                                                                                                                                                                                                                                                                                                                                                           ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82 TISVAIDVTNVYIMGYRAGDISYFF---NEASATEAAKYVFKDAKRKVTLPYSGNYERLQ 138
                                                                                                                                                                          123
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                                                                                                                                                                                                                                                                                                       31 LEDNNIFPKQY-PIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVL--PNRVGLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IAAGKIRENIPLG
                                                                                                                                                                                                                               --NQYVTVELSYSDTVSIQLGIDLTNAYVVAYRAGSESFFF---RNAPASASTYLFTGTQ
                                                                                                                                                                                                                                                                                       LHGNAYYQAQFQDPIKFTTGSATPASYNQFIDALRERLTGG--LIYGIPVLRDPSTVEKP
                                                                                                                                                                                                     NRYTFAFGGNYDRLEQLAGNLRENIELG 175
                                                                                                                                                                                                                                                          INQRFILVELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQ
                                                                                                                                                                          -QYSLPFDGNYDDLEKWAHQSRQRISLG
                                                                                                                                                                                                                                                                                                                                                                                                     Toxin. 547 AA; 61248 MW; 355A325C2354A1BD CRC64;
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                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                     PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                            26.2%; Score 248.5; DB 1 43.9%; Pred. No. 4.1e-15; tive 21; Mismatches 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _B_lectin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151
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                                                                                                        PRT;
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                                                                                                                                                                              149
                                                                                                        251 AA.
                                                                                                                                                                                                                                                                                                                                                                            DB 10;
                                                                                                                                                                                                                                                                                                                                                  51; Indels 11; Gaps
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Best Local Similarity
Matches 60; Conserv
                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                    Hydrolase; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3816;
                                          117 ERWAHQSRQQIPLG 130
                                                              162 EQLAGNLRENIELG 175
                                                                                                    104 SVTLALDVTNAYVVGYRAGNSAYFFH---PDNQEDAEAITHLFTDVQNRYTFAFGGNYDRL 161
                                                                                63 SIEVGIDVTNAYVVAYRAGTQSYFLRDAPSSASD----YLETGT-DQHSLPFYGTYGDL 116
                                                                                                                                       44 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLDNRVGLPINQRFILVELSNHAEL 103
                                                                                                                          5 IKFSTEGATSQSYKQFIEALRERLRGG--LIHDIPVLPDPTTLQERNRYITVELSNSDTE 62
                                                                                                                                                                     ch 25.8%; Score 245; DB 10; Length 251; 1 Similarity 44.8%; Pred. No. 3.1e-15; 60; Conservative 18; Mismatches 46; Indels 10;
                                                                                                                                                                                                                     251 ;
251 AA;
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; 27997 MW;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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US-08-218-303-16
US-08-338-793D-61
US-09-538-873-1
US-09-538-873-1
US-08-485-266-77
US-08-485-1138-6
US-08-485-1385-6
US-08-48-7-4848-6
US-08-839-755-6
US-09-610-838-6
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US-08-477-484B-1
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US-08-839-765-1
US-09-136-389-1
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PCT-US92-09487-1
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ALIGNMENTS	US-08-597-731-2	US-08-245-754A-2	US-08-902-486-7	PCT-US92-09487-6	US-08-425-336-6	US-07-988-430-6	US-07-901-707-6	US-09-538-873-3	US-08-485-286-71	US-08-378-761A-71	US-08-324-301-15	US-09-726-651A-4	US-08-483-502-4	US-08-484-341-4	US-08-482-920-4	US-08-184-237-4	US-07-923-692C-4	US-08-485-286-74
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RESULT 1 US-07-901-707-1

#### ; TOPOLOGY: 1: ; MOLECULE TYPE: US-07-901-707-1 Sequence 1, Application US/07901707 Patent No. 5376546 APPLICATION NÜMBER: US/07/901,707 FILING DATE: 19920619 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 07/787,567 FILING DATE: 04-NOV-1991 ATTORNEY/AGENT INFORMATION: NAME: NO. 5376546and, Greta E. REGISTRATION NUMBER: 35,302 REFERENCE/DOCKET NUMBER: 27129/3091 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: GENERAL INFORMATION: INFORMATION FOR SEQ ID NO: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: ISM PC Compatible OPERATING SYSTEM: PC POS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: SEQUENCE CHARACTERISTICS: LENGTH: 267 amino acids TYPE: AMINO ACID APPLICANT: Better, Marc D. APPLICANT: Carroll, Steve F. APPLICANT: Lane, Julie A. TITLE OF INVENTION: Materials Comprising and Methods of TITLE OF INVENTION: Composition and Use for Ribosome-Inactivating Proteins NUMBER OF SEQUENCES: 57 CORRESPONDENCE ADDRESS: APPLICANT: Bernhard, APPLICANT: Better, M STREET: TWO First National Plaza, 20 South Clark STREET: Street CITY: Chicago STATE: Illinois TELEFAX: (312) 984-5750 TELEX: 25-3856 COUNTRY: ADDRESSEE: 60603 USA Marshall, O'Toole, Gerstein, Murray & Bicknell protein Susan L. 27129/30910

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                                                                                                   INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 07/787,567
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: No. 5416202and, Greta E.
REGISTRATION NUMBER: 35302
REGISTRATION NUMBER: 35302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Materials Comprising and Methods of TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins NUMBER OF SEQUENCES: 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
              MOLECULE TYPE: protein
                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acid
                                                                                                                                                  REFERENCE/DOCKET NUMBER: 31133
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0.
                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 19921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Chicago
STATE: Illinois
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                              TYPE: AMINO ACID TOPOLOGY: linear
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                                                                                                                     25-3856
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                                                           267 amino acids
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Lei, Shau-Ping
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                                                                                                                                    (312) 984-9740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bernhard,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Susan L.
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; Mismatches 0;
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                               ; MOLECULE TYPE: US-08-425-336-1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1,
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                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Thomas C.
                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Carroll, Stephen F. APPLICANT: Studnika, Gary M.
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                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                    TELEFAX: 25-3856
                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 07/901,707 FILING DATE: 19-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 12-MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/425,336 FILING DATE: 18-APR-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                  TOPOLOGY:
                                                                                               LENGTH:
                                                                                                                                                                                                                                           REGISTRATION NUMBER: P-36,989
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                                                                                amino acid
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                                                                                               267 amino acids
                                                                                                                                                                       312/474-0448
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                                            protein
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                                                                                                                                                                                                                                                                                                                                                                                                      08/064,691
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Pred. No. 1.7e-111;
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Length 267;
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Query Match

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Score 1020;

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US-08-488-113B-1
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                             TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                  APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                        APPLICATION NUMBER: 19-JUN-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
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CITY: Chicago
CTATE: Illinois
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                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 09-DEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/488,113B FILING DATE: 07-JUN-1995 CLASSIFICATION: 530
                                                                  TELEX:
                                                                                 TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
                                                                                                                                 REFERENCE/DOCKET NUMBER: 11022US07/200-70.P3.C2A
                                                                                                                                               REGISTRATION NUMBER: 32,918
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 18-API
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: PatentI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                    McNicholas, Janet M
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              267 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Studnika,
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                                                                                                                                                                                                                                                          19-JUN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunotoxins Comprising Ribosome-Inactivating
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REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 111
TELECOMMUNICATION INFORMATION:
                                                   FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNICHOLAS, Janet M
                                                                                                                       FILING DATE: 19-JUN-PRIOR APPLICATION DATA:
                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
FILING DATE: 18-APR-1995
                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                         APPLICATION NUMBER:
                                                                                                                                                         APPLICATION NUMBER: US 07/901,707
                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 0 FILING DATE: 12-MAY-1993
                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 500 We CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/477,484B FILING DATE: 07-JUN-1995
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                                                                                                       US 07/787,567
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                  11022US07/200-70.P3.C2A
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Pred. No. 1.7e-111;
0; Mismatches 0;
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TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
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Patent No. 5837491
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                                                                    PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/
FILING DATE: 09-DEC-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                             CURRENT AFFLICATION NUMBER: US/08/540,500
APPLICATION NUMBER: 13-MAY-1996
FILING DATE: 13-MAY-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/US94/05348
                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxir
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                 APPLICATION NUMBER: US 0: FILING DATE: 19-JUN-1992 PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 500 We CITY: Chicago
                                                                                                                                                                                                       APPLICATION NUMBER: PCT/I
FILING DATE: 12-MAY-1994
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APPLICATION NUMBER:
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500 West Madison Street, 34th floor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                    US 08/064,691
                                                                                                               US 07/988,430
                                                        US 07/901,707
US 07/787,567
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US-08-839-765-1
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Best Local Similarity
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
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ATTORNEY/AGENT INFORMATION:
NAME: MCNICholas, Janet M.
REGISTRATION NUMBER: 32,91
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LENGTH: 267 amino acids
                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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PRIOR APPLICATION DATA:
08/425,336
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                            FILING DATE: 12-MAY-PRIOR APPLICATION DATA:
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TELEFAX: 312/707-9155
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                                                                                                                                                              APPLICATION NUMBER: US 0: FILING DATE: 18-APR-1995
                                                                                                                                                                                                                                                                FILING DATE: 15 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/839,765 FILING DATE: 15-APR-1997
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APPLICATION NUMBER:
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ER: 200-70.P4
US 07/988,430
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Pred. No. 1.
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Best Local (
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INFORMATION FOR SEQ ID NO: 1:
                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
              CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                       APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                             APPLICANT:
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LENGTH: 267 amino acid
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TELEPHONE: 312/707-8889
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ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
                                           FILING DATE:
                                                                                                                                                                                                STREET: 500 We CITY: Chicago
  APPLICATION NUMBER:
                                                       APPLICATION NUMBER:
                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                     STATE:
                                                                                                                                                                                                                            ADDRESSEE:
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REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US09/200-70.p3.C3
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GY: linear
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                                                                                                                                                                                    Illinois
                                                                                                                                                                                                          500 West Madison Street, 34th floor
                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                             Better, Marc D.
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                                                                                                                                                                                                                                                                      Proteins
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08/646,360
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                                                       US/09/136,389
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US-09-610-838-1
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                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09610838 Patent No. 6376217
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Best Local Similarity
                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                             STREET: Chicago
CITY: Chicago
TATE: Illinois
                                                                                                                                                                                                                                         APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
                                                                                                                                                                                         TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: US 0
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
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                                                                                                                                500 West Madison Street, 34th floor
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312/707-9155
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PCT-US92-09487-1
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                                                                                                              Sequence 1, Application PC/TUS9209487 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 1:
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FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/064,691
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               APPLICANT: Lane, Julie A. APPLICANT: Lei, Shau-Ping TITLE OF INVENTION: Mater:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acid
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TITLE
                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: MCNicholas, Janet M. REGISTRATION NUMBER: 32,918 REFERENCE/DOCKET NUMBER: 200
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 OF INVENTION:
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                                                Carroll, Stephen F.
Lane, Julie A.
                                                                                 Bernhard, Susan L.
Better, Marc D.
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Materials Comprising and Methods of Preparation and Use for Ribosome-Inactivating Proteins
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US-08-356-786-8
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                                                       APPLICANT:
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Sequence 8, Application US/08356786 Patent No. 5877305
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APPLICATION NUMBER: US 07/
FILING DATE: 19-UUN-1992
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 07/
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMETION:
                                                                                          GENERAL INFORMATION:
APPLICANT: Huston
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TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
APPLICANT: Ring, David B.
TITLE OF INVENTION: Biosyl
TITLE OF INVENTION: Market
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Two First National Plaza, 20 South Clark STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (314) 984-9740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Noland, Greta E. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                     181 FQYIEGEMRTRIRYNRRS 198
                                                                                                                                                                                                                                    181 FQYIEGEMRTRIRYNRRS 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Chicago
: Illinois
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                                                                           Oppermann, Hermann
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                         Houston, L.
                                                                                            Huston, James S.
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         Marker
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                       Biosynthetic Binding Protein for Cancer
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                                                                                                                                                                               Sequence 27, Application US/08378761A Patent No. 5635384 GENERAL INFORMATION:
APPLICANT: WALSH, TERENCE A
                                                                        APPLICANT: WALSH, TERENCE A
APPLICANT: HEY, TIMOTHY D
APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-1
TITLE OF INVENTION: PRECURSOR
NUMBER OF SEQUENCES: 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (617) 248-7100 INFORMATION FOR SEQ ID NO: (
                           CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: CR. TELECOMMUNICATION INFORMATION: TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PATIOR APPLICATION DATA:
APPLICATION NUMBER: 07/831,967
FILING DATE: 06-FEB-1992
FITCHEY/AGENT INFORMATION:
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APPLICATION NUMBER: US/08/356,786
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ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibeault
STREET: Exchange Place, 53 State Street
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Pitcher, Edmund R. REGISTRATION NUMBER: 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
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                                                                                              RIBOSOME-INACTIVATING PROTEINS, INACTIVE PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF USING
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RESULT 13
US-08-485-286-27
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Patent No. 5646026 5646119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                            APPLICANT: WALSH, TERENCE A
APPLICANT: WALSH, TENOCHY D
APPLICANT: HEY, TIMOCHY D
APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF
TITLE OF INVENTION: USING
CURRENT APPLICATION DATA:
                                                              MEDIUM TYPE: Floppy
                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDREA T. BORUCKI
                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: protein
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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TELECOMMUNICATION INFORMATION:
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NAME: BORUCKI, ANDREA T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                    COUNTRY:
                                                                                                                                        STATE:
                                                                                                                                                                    STREET:
                                                                                                                                                     CITY: INDIANAPOLIS
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          PatentIn Release #1.0, Version #1.25
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 Mismatches

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CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Patent No.
                                                                                                                                                                                                                                                                                                          SEQ ID NO:4:
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Best Local Similarity
                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08 FILING DATE: 26-JAN-1995 ATTORNEY/AGENT INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: WALSH, TERENCE A.; HEY, TIMOTHY D.; MORGAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                        LENGTH: 290
                                                                                                                                                                                                                                                                                                                          FILING DATE: 11-JUN-1990
                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       atch 100.0%; score 1020; DB 1; cal Similarity 100.0%; Pred. No. 1.9e-111; 198; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 GNYDRLEOLAGNI.RENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 180
                                121 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 180
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                                                                                                                                   25 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 84
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                                                                                                                                                       1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 60
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 FQYIEGEMRTRIRYNRRS 222
                                                                  ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 144
                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                    100.0%; Score 1020; DB 6;
100.0%; Pred. No. 1.9e-111;
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                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (617) 248-71
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/356,786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Blosynt TITLE OF INVENTION: Marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: CR
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 07/8: FILING DATE: 06-FEB-1992 ATTORNEY/AGENT INFORMATION: NAME: Pitcher, Edmund R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                 LENGTH: 534 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
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                                                        198;
184 FQYIEGEMRTRIRYNRRS 201
                                                                                                                        64
                                                                                                                                   61 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFFPDNQEDAEAITHLFTDVQNRYTFAFG 120
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                                                                                                                     ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                           FOYIEGEMRTRIRYNRRS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Edmund R. Pitcher, Testa, Hurwitz, & Thibeault Exchange Place, 53 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Houston, L. L.
Ring, David B.
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                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                               248-7100
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                                                                                                                                                                                                                                                          100.0%; Score 1020; DB 2; 100.0%; Pred. No. 4.8e-111;
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Search completed: September 16, 2003, 11:51:46

Job time : 11.2796 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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1: /cgn2_6/ptodata/2/pubpaa/U
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US-10-282-935-1
US-09-792-793A-39
US-09-792-793A-39
US-10-127-890-6
US-10-280-679B-4
US-10-282-935-3
US-935-34
US-10-127-890-7
US-10-127-890-7
US-10-127-890-5
US-10-127-890-110
US-10-127-890-111
US-10-127-890-101
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US-09-347-064-8
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1439.723 Million cell updates/sec
             Sequence 2, Appli
Sequence 8, Appli
Sequence 5, Appli
Sequence 110, App
Sequence 111, App
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                                                                                                                                            Sequence 1, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 6, Appli
Sequence 4, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 7, Appli
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124	124	124	124	125	126	135	135	135	135	176	176	180.5	182	182	240.5	241.5	241.5	241.5	241.5	242.5	242.5	242.5	242.5	242.5	242.5	243.5	243.5	244.5	244.5
12.2	12.2	12.2	12.2	12.3	12.4	13.2	13.2	ω	ω.	17.3	17.3	17.7	17.8	7.	23.6	23.7	23.7	23.7	·	ω.	ω.	23.8	ω.	ω	ω.	ω	ω	4	24.0
327	275	259	254	332	330	280	280	280	280	250	250	261	314	263	251	332	309	293	251	251	251	251	251	251	251	251	251	251	251
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79,	35,	10,		73,	82, A	129,	128	127	ω.	_	ω,	۰.	Sequence 2, Appli		e 108	Sequence 251, App	253	259.	109,	105,	104		102,	m .	247		100.	107.	Sequence 99, Appl

#### ALIGNMENTS

RESULT 1 US-10-127-890-1

Sequence 1, Application US/10127890 Publication No. US20030166196A1 GENERAL INFORMATION:

APPLICANT: Better, Marc D.

Carroll, Stephen F.

Studnika, Gary M.

FITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating Proteins

NUMBER OF SEQUENCES: 173

CORRESPONDENCE ADDRESS:
ADDRESSE: McAndrews, Held & Mailoy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Tlops/MS-DOS
SOFWARR: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION NUMBER: US/10/127,890
FILING DATE: 3-Apr-2002
CLASSIFICATION NUMBER: US/10/127,890
FILING DATE: 12-MAY-1996
APPLICATION NUMBER: US/08/646,360
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US/08/646,360
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US/08/64,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 11-US/08/646,360
FILING DATE: 19-DEC-1992
APPLICATION NUMBER: US 07/988,430
FILING DATE: 19-JUN-1992

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FILE REFERENCE: UTSD:884US
CURRENT APPLICATION NUMBER: US/10/282,935
CURRENT FILING DATE: 200-10-29
PRIOR APPLICATION NUMBER: 09/538,873
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/126,826
PRIOR APPLICATION NUMBER: 60/126,826
PRIOR FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 1
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Publication No. US20030143193A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Matches 196;
                     Best Local Similarity
                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: VITETTA, ELLEN S.
APPLICANT: GHETIE, VICTOR F.
APPLICANT: SMALLSHAW, JOAN
APPLICANT: SMALLSHAW, JOAN
APPLICANT: BALUNA, ROXANA G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF TITLE OF INVENTION: PROTEINACEOUS COMPOUNDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 312/707-9155
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
                                                                                                   OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Peptide
                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                               TYPE: PRT
                                                                                                                                           FEATURE:
                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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LENGTH: 267 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 IFPKOYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 60
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REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/787,567 FILING DATE: 04-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; ilarity 100.0%; Conservative 0
  Conservative
                   100.0%;
                     99.0%; Score 1010; DB 12; 100.0%; Pred. No. 9.9e-108;
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Pred. No. 7e-109;
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    Mismatches
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                                        Length 267;
    Indels
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US-10-127-890-6
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 39
LENGTH: 247
TYPE: PRT
ORGANISM: Trichosanthews kirilowii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: McDonald, John R.
APPLICANT: Coggins, Philip
APPLICANT: Coggins, Philip
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
FILE REFERENCE: 25020-601D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 39, Application US/09792793A Patent No. US20020168370A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/792,793A CURRENT FILING DATE: 2001-02-22
                                                                                                                                                                                                           GENERAL INFORMATION:
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             CORRESPONDENCE ADDRESS:

ADDRESSEE: McAndrews, Held & Malloy, Ltd.

STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                     TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                     APPLICANT: Better, Marc D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 YIEGEMRTRIRYNRRS 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                              116 TAAGKIRENIPLGLPALDSAITTLFYYNAN----SAASALMVLIQSTSEAARYKFIEQQ
                                                                                                                                                                                                                                                                                                                                                             171 IGKRV 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VSFRLSGATSSSYGVFISNLRKALPNERKL-YDIPLL--RSSLPGSQRYALIHLTNYADE 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 33.5%; Score 342; DB 10; Similarity 39.5%; Pred. No. 5.6e-31;
CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                 Carroll, Stephen F.
                                                                                                                                         Studnika, Gary M.
                                                                                                     Proteins
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US-10-280-679B-4
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                                                                                                                       Sequence 4, Application US/10280679B Publication No. US20030150019A1 GENERAL INFORMATION:
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Best Local (
APPLICANT: Large Scale Biology Corporation
TITLE OF INVENTION: Monopartite RNA Virus Transformation Vectors
FILE REFERENCE: LSBC-0109-US03
CURRENT APPLICATION NUMBER: US/10/280,679B
CURRENT FILING DATE: 2000-10-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 312/707-9155
TELEX: 650 388 1248
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 247 amino acids
TYPE: amino acid
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FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNICHOLAS, Janet M.
REGISTRATION NUMBER: 32,918
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
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FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                    171 IGKRV 175
                                                                                                                                                                                                                                                                                                                                                                                                               128 QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 187
                                                                                                                                                                                                                                                                                                                                                  188 MRTRI 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 TISVAIDVTNVYIMGYRAGDTSYFF---NEASATEAAKYVFKDAMRKVTLPYSGNYERLQ 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VSFRLSGATSSSYGVFISNLRKALPNERKL-YDIPLL--RSSLPGSQRYALIHLTNYADE 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       n 33.5%; Score 342; DB 12; Length 247; Similarity 39.5%; Pred. No. 5.6e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYTLALDYTNAYVYGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/646,360 FILING DATE: 13-MAY-1996 APPLICATION NUMBER: PCT/US94/05348 FILING DATE: 12-MAY-1994 APPLICATION NUMBER: US 08/064,691 FILING DATE: 12-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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CURRENT APPLICATION NUMBER: US/10/282,935
CURRENT FILING DATE: 2002-10-29
PRIOR APPLICATION NUMBER: 09/538,873
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/126,826
PRIOR APPLICATION NUMBER: 60/126,826
PRIOR FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 3
LENGTH: 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/10282935
Publication No. US20030143193A1
GENERAL INFORMATION:
APPLICANT: VITETTA, ELLEN S.
APPLICANT: GHETIE, VICTOR F.
APPLICANT: SMALLSHAW, JOAN
APPLICANT: SMALLSHAW, JOAN
APPLICANT: SMALLSHAW, JOAN
APPLICANT: SMALLSHAW, JOAN
APPLICANT: MALLSHAW, JO
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US-10-282-935-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: BALUNA, ROXANA G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
TITLE OF INVENTION: PROTEINACEOUS COMPOUNDS
FILE REFERENCE: UTSD:884US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local Similarity 39.5%; Score 342; DB 1
Best Local Similarity 39.5%; Pred. No. 7e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 4
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PRIOR FILING DATE: 1988-02-26
PRIOR APPLICATION NUMBER: 07/160,771
PRIOR FILING DATE: 1988-02-26
TYPE: PRT
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PRIOR FILING DATE: 2000-04-24
PRIOR APPLICATION NUMBER: 08/484,341
PRIOR FILING DATE: 1995-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Chinese cucumber protein alpha-trichosanthin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 07/923,692 PRIOR FILING DATE: 1992-07-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1991-07-26
APPLICATION NUMBER: 07/739,143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188 MRTRI 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       128 OLAGNIRENIEIGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 187
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                                                                                                          US-10-127-890-4
                                                                                                                              RESULT 8
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Best Local Similarity
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SEQ ID NO 34
LENGTH: 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                         Sequence 4, Application US/10127890 Publication No. US20030166196A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: McDonald, John R.
APPLICANT: Coggins, Philip
TITLE OF INVENTION: MCTHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE AND
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
FILE REFERENCE: 25020-601D
CURRENT APPLICATION NUMBER: US/09/792,793A
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Bryonia dioica
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                       APPLICANT: Better, Marc D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             117 ERWAHQSRQQIPLGLQALTHGIS---FFRSGGNDNEEKARTLIVIIQMVAAAARFRYISN 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187
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                                                                                                                                                                                                                                                                         116 TAAGKIRENIPLGLPALDSAITTLYYYTAS----SAASALLVLIQSTAESARYKFIEQQ 170
                                                                                                                                                                                                                                                                                                              128 QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 187
                                                                                                                                                                                           171 IGKRV 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69 SYTLALDYTNAYYVGYRAGNSAYFFH--PDNQEDAEAITHLFTDVQNRYTFAFGGNYDRL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ch 31.7%; l Similarity 42.2%; 79; Conservative 2
                                                                                                                                                                                                                                                                                                                                                            59 TISVAVDVTNVYIMGYLAGDVSYFF---NEASATEAAKFVFKDAKKKVTLPYSGNYERLQ 115
                                                                                                                                                                                                                                                                                                                                                                                                 69 SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                           2 VSFRLSGATTTSYGVFIKNLREALPYERKV-YNIPLL--RSSISGSGRYTLLHLTNYADE 58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
Carroll, Stephen F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30.6%; Score 312; DB 10; 37.3%; Pred. No. 1.6e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28; Mismatches
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Pred. No. 7.7e-29;
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US-10-127-890-4
RESULT 9
US-10-127-890-7
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Best Local !
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US/08/646,360
RILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 08/064,691
FILING DATE: 09-DEC-1993
APPLICATION NUMBER: US 07/988,430
APPLICATION NUMBER: US 07/981,707
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 19-UN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNICHOLAS, Janet M.
REGISTRATION NUMBER: 32,918
ATTORNEY/AGENT SIMPLES SIMPLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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ADDRESSEE: McAndrews, Held & Malloy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Immunotoxins Comprising Ribosome Inactivating
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
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                                                                                                                                                                                                                                                                                                                                                  115 AAHKIRENIDLGLPALSSAITTLFYYNA-----QSAPSALLVLIQTTAEAARFKYIERHV 169
                                                                                                                                                                                                                                                                                                                                                                                                         129 LAGNILRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEM 188
                                                                                                                                                                             170 AKYVATN 176
                                                                                                                                                                                                                                                                         189 RTRIRYN 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             69 SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQ 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      60661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.4%; Score 279; DB 12; 35.3%; Pred. No. 1.1e-23;
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TOPOLOGY: Inear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-127-890-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 09-USC-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 09-007/787,567
FILING DATE: 04-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: 312/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: MCN1cholas, Janet M.
REGISTRATION NUMBER: 32,918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
170 QIQER 174
                                             187 EMRTR 191
                                                                           115 QIAAGKPREKIPIGLPALDSAISTLLHYDS----TAAAGALLVLIQTTAEAARFKYIEQ 169
                                                                                                                      127 EQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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                                                                                                                                                                 58 KTITVAVDVTNVYIMGYLADTTSYFF---NEPAAELASQYVFRDARRKITLPYSGNYERL 114
                                                                                                                                                                                           68 LSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAE-AITHLFTDVQNRYTFAFGGNYDRL 126 ::|:|:|| | ::| | : | | :|| | 126
                                                                                                                                                                                                                                                      2 VSFRLSGADPRSYGMFIKDLRNALPFREKV-YNIPLLLPSVSGA---GRYLLMHLFNYDG 57
                                                                                                                                                                                                                                                                                               9 INFTTAGATYQSYTNFIRAVRGRLTTGADVRHEIP-VLPNRVGLPINQRFILVELSNHAE 67
                                                                                                                                                                                                                                                                                                                                                        68;
                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 263 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/10/127,890 FILING DATE: 23-Apr-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 312/707-9155
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STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carroll, Stephen F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3E: McAndrews, Held & Malloy, Ltd. 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                             27.2%; Score 277; DB 12; 36.8%; Pred. No. 1.8e-23; tive 41; Mismatches 62;
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US-09-347-064-2
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; SEQ ID NO 2
TWICTH: 252
                        NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2
SEQ ID NO 8
LENGTH: 252
TYPE: PRT
                                                                                                                                                               APPLICANT: Eck, Jurgen
APPLICANT: Schmidt, Arno
APPLICATION: Ribosome-Inactivating Proteins of the mistletoe Viscum
TITLE OF INVENTION: Album
FILE REFERENCE: 09282-5
CURRENT ENVENTION: NUMBER: US/09/347,064A
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: PCT/EP98/00009
EARLIER APPLICATION NUMBER: PCT/EP98/00009
EARLIER APPLICATION NUMBER: PCT/EP98/00009
EARLIER APPLICATION NUMBER: PCT/EP98/00009
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Application US/09347064A Patent No. US20020045208A1
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                                                                                                                                                     EARLIER FILING DATE: 1997-01-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Eck, Jurgen
APPLICANT: Schmidt, Arno
APPLICANT: Zinke, Holger
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EARLIER FILING DATE: 1998-01-02
EARLIER APPLICATION NUMBER: EP 97 10 0012.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Recombinant Fusion Proteins Based on TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe Viscum TITLE OF INVENTION: album
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER FILING DATE: 1997-01-02 NUMBER OF SEQ ID NOS: 38
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ORGANISM: Viscum album
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 YINSGASFLPDVYMLELETSWGQQSTQVQHS 210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 GH-RDQIPLGIDQLIQSVTALRF---PGGSTRTQARSILILIQMISEAARFNPILWRARQ 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131 GNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARF------Q 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 TAAIDVTNLYVVAYQAGDQSYFLR-DAPRGAE--THLFTGT-TRSSLPFNGSYPDLERYA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13 TAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPIN--QRFILVELSNHAELSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 TLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38;
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Indels Length 248;

11;

Gaps

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US-10-127-890-5
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  TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Studnika, Gary M. TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Better, Marc D.
SEQUENCE
                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 GH-RDQIPLGIDQLIQSVTALRF----PGGSTRTQARSILILIQMISEAARFNPILWRARQ 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 GNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARF------- 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     183 YIE-----195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13 TAGATVOSYTNEIRAVRGRLTTGADVRHEIPVLPNRVGLPIN--QREILVELSNHAELSV 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 TAAIDVINLYVVAYQAGDQSYFLR-DAPRGAE--THLFTGT-TRSSLPFNGSYPDLERYA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 TLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 Similarity 79; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9 THQTTGEEYFRFITLLRDYVSSGS-FSNEIPLL-RQSTIPVSDAQRFVLVELTNQGGDSI 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YINSGASFLPDVYMLELETSWGQQSTQVQHS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 23-Apr-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: PCT/US94/05348 FILING DATE: 12-MAY-1994 APPLICATION NUMBER: US 08/064,691 FILING DATE: 12-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Chicago
                                                                     TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
                                                                                                                                                                                                                            APPLICATION NUMBER: US 07/787,567 FILING DATE: 04-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/646,360 FILING DATE: 13-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 60661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
                                                                                                                                        REFERENCE/DOCKET NUMBER: 200-70.P4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/10/127,890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carroll, Stephen F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 276; DB 9; Length 252; Pred. No. 2.2e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38;
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US-10-127-890-110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best
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TYPPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Better, Marc D. Carroll, Stephen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
           TELECOMMUNICATION INFORMATION:
                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         116 AAGKIREKIPLGFPALDSALTTIFHYDS----TAAAAAFLVILQTTAEASRFKYIEGQI 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     129 LAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARPQYIEGEM 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        171 IERISKNQ 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  189 RTRIRYNR 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 AITVAVDVSQLYIMGYLVNSTSYFF---NESDAKLASQYVFKGSTIVTLPYSGNYEKLQT 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69 SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQ 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 VRFSLSGSSSTSYSKFIGDLRKALPSNGTVYNLTILLSSASGA---SRYTLMTLSNYDGK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                  NAME: MCNicholas, Janet M. REGISTRATION NUMBER: 32,918 REFERENCE/DOCKET NUMBER: 200-70.P4
                                                                                                                                                               APPLICATION NUMBER: US 07/988,430 FILING DATE: 09-DEC-1992 APPLICATION NUMBER: US 07/901,707 FILING DATE: 19-JUN-1992
                                                                                                                                                                                                                                                          FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                   APPLICATION NUMBER: US 07/787,567 FILING DATE: 04-NOV-1991
                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/646,360 FILING DATE: 13-MAY-1996
                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US94/05348
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 267.5; DB 12; Pred. No. 2.1e-22;
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TOPOLOGY: linear;
; MOLECULE TYPE: protein;
; SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-127-890-110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Poca T
                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                     APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: CUNKNOWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 60661
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Better, Marc D.
Carroll, Stephen F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 LAEIAIDVTSVYVVGYQVRNRSYFFKDAPD-----AAYEGLFKNTIKTR--LHFGGSYPS 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 SYTLALDYTNAYVVGYRAGNSAYFFH--PDNQEDAEAITHLFTD-VQNRYTFAFGGNYDR 125
                                APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                   APPLICATION NUMBER: US/08/646,360 FILING DATE: 13-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: McAndrews, Held & Malloy, Ltd. STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IENQIRNNFQQRIR 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IEGEMRT----RIR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LE---GEKAYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTF 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 312/707-9155
TELEX: 650 388-1248
   APPLICATION NUMBER: US 07/787,567 FILING DATE: 04-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 312/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/10127890 o. US20030166196A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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37.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proteins
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Pred. No. 5.5e-20;
""" matches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     110:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 12;
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US-10-127-890-101
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Best Local Similarity
Watches 72; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-127-890-111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 101, Application US/10 Publication No. US20030166196A1 GENERAL INFORMATION:
                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 17 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173 IENQIRNNFQQRIR 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       184 IEGEMRT----RIR 193
                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                  STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                   CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX:
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TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 111:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 111:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 312/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116 LE---GEKAYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARFTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          126 LEQLAGN--LRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQY 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 LAEIAIDVTSVYVVGYQVRNRSYFFKDAPD-----AAYEGLFKNTIKTR--LHFGGSYPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 SYTLALDYTNAYVYGYRAGNSAYFFH--PDNQEDAEAITHLFTD-VQNRYTFAFGGNYDR 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9 INFTTAGATYQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 VSFSTCGATYITYVNFLNELRVKLKPEGN-SHGIPLLRKKADDP-GKAFVLVALSNDNGQ 62
                                                                                                                                                                                                                    APPLICATION NUMBER: US/10/127,890 FILING DATE: 23-Apr-2002 CLASSIFICATION: <Unknown>
                          APPLICATION NUMBER: US 08/064,691 FILING DATE: 12-MAY-1993
                                                                                 APPLICATION NUMBER: PCT/US94/05348 FILING DATE: 12-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: McAndrews, Held & Malloy, Ltd. STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: McNicholas, Janet M. REGISTRATION NUMBER: 32,91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 200-70.P4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 251 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Better, Marc D.
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US 07/988,430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 246.5; DB 12; Pred. No. 5.5e-20;
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Search completed: September 16, 2003, 12:09:56 Job time : 21.4768 secs
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APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNICholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acid
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                           Query Match 24.1%; Score 245.5; DB 12; Length 251; Best Local Similarity 37.1%; Pred. No. 7.2e-20; Matches 72; Conservative 31; Mismatches 70; Indels 21;
                                                                                                                               173 IENQIRNNFQQRIR 186
                                                                                                  184 IEGEMRT----RIR 193
                                                                                                                                                                                              21; Gaps
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on:

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
               930.5
353.5
353.5
345
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
               BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              283308 seqs, 96168682 residues
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1020
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length DB
               RLCSD
RLCSAG
S32431
S16022
S348002
RLTZT
JU0393
JU55036
JU55036
JU55036
C39761
C39761
C39761
C39761
S262494
S33519
JN0108
S262494
S27494
S2749
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abrin-a precursor
beta-luffin - smoot
luffin-b - smoot
agglutinin I precu
mistletoe lectin I
rRNA N-glycosidase
precion of the complete of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                agglutinin precurs
abrin-d precursor
abrin-b precursor
abrin-b precursor
rRNA N-glycosidase
karasurin - Mongol
karasurin - G - Tric
karasurin C - Tric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           abrin (clone 7.2)
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Result No.

Database

					_		-		36			-			_
110	110.5	111	111	111	115	121	122	123	123.5	124	127	127	131	132	133
10.8	10.8	10.9	10.9	10.9	11.3	11.9	12.0	12.1	12.1	12.2	12.5	12.5	12.8	12.9	13.0
236	318	319	319	319	253	292	310	253	293	283	253	253	253	280	281
ν	Ν	N	N	2	2	-	N	N	N	N	ນ	N	ν	Ν	2
S17932	S01032	G85640	E90779	I54695	A58923	RLQHG2	S46239	S28541	S17519	S05205	S29931	S28539	S28542	JC5848	в38664
rRNĀ N-glycosidase	-like	Shiga toxin 2 subu	Shiga toxin 2 subu	shiga-like toxin I	rRNA N-glycosidase	rRNA N-glycosidase	ribosome-inactivat	rRNA N-glycosidase	protein synthesis	30K ribosome inact					

## ALIGNMENTS

A;Title: Revised amino acid sequence of the B-chain of ricin D due to loss of tryptop A;Reference number: A24010 A;Recession: A24010 A;Molecule type: protein A;Residues: 315-383,'ps',386-576 <ara> R;Funatsu, G.; Kimura, M.; Funatsu, M. Agric. Biol. Chem. 43, 2221-2224, 1979 A;Title: Primary structure of Ala chain of ricin D. A;Reference number: A03374 A;Accession: A03374 A;Molecule type: protein</ara>	A; Molecule type: mRNA A; Residues: 12-75, 'D',77-550,'R',552-576 <lam> A; Residues: 12-75, 'D',77-550,'R',552-576 <lam> A; Cross references: GB:X02388; NID:g21077; PIDN:CAA26230.1; PID:g21078 A; Cross references: GB:X02388; NID:g21077; PIDN:CAA26230.1; PID:g21078 A; Cross references: GB:X02388; NID:g2107; PIDN:CAA26230.1; PID:g21078 A; Cross reference description and sequences of peptic peptides, and the complete sequence of Ile A; Reference number: A03372 A; Reference number: A03372 A; Rocession: A03372 A; Rocession: A03372 A; Rocession: A03372 A; Roceule type: protein A; Residues: 36-97, 'Q',99-109, 'S',111-269, 'D',272-283, 'L',285-288,290-302 <vos> A; Note: this paper cites the others in the series providing experimental details for F2BS Lett. 191, 121-124, 1985</vos></lam></lam>	A; Accession: A24041 A; Molecula type: DNA A; Residues: 1-576 <hal> A; Rosidues: 1-576 <hal> A; Cross-references: GB:X03179; NID:g21082; PIDN:CAA26939.1; PID:g21083 A; Cross-references: GB:X03179; NID:g21082; PIDN:CAA26939.1; PID:g21083 A; Tregear, J.W.; Roberts, L.M. Plant Mol. Biol. 18, 515-525, 1992 A; Title: The lectin gene family of Ricinus communis: cloning of a functional ricin ge A; Reference number: 820513; MUID:92163016; PMID:1371405 A; Reference number: A24614; MUID:921084; PIDN:CAA37095.1; PID:g21085 A; Reference number: A24614; MUID:95179479; PMID:3838723 A; Accession: A24614 A; MUID:85179479; PMID:3838723 A; Accession: A24614</hal></hal>	RESULT 1  RLCSD  RLCSD  RLCSD  RICII D precursor - castor bean  N;Contains: rRNA N-glycosidase (EC 3.2.2.2)  C;Species: Ricinus communis (castor bean)  C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999  C;Accession: A24041; S20513; A24614; A03372; A24010; A03374; S10903  R;Halling, K.C.; Halling, A.C.; Murray, E.E.; Ladin, B.F.; Houston, L.L.; Weaver, R.F  Nucleic Acids Res. 13, 8019-8033, 1985  A;Title: Genomic cloning and characterization of a ricin gene from Ricinus communis.  A;Reference number: A24041; MUID:86067214; PMID:2999712

```
F:46-293/Domain: rRNA N-glycosidase homology KRNG>
F:315-576/Product: ricin D chain B #status experimental <BCH>
F:315-576/Product: ricin D chain B #status experimental <BCH>
F:315-373,374-414,417-455,462-497,501-540,543-576/Region: 40-residue repeats
F:45,409,449/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:115,158,243,244/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F:212/Active site: Glu #status experimental
F:215/Active site: Arg #status predicted
F:294-318,334-353,377-394,465-478,504-521/Disulfide bonds: #status experimental
F:336,349,360/Binding site: N-acety/galactosamine (Asp, Gln, Asn) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Contents: annotation; X-ray crystallography, 2.5 angstroms
C;Comment: The functional molecule is a disulfide-linked dimer of A and B chains, which
C;Comment: The A chain inhibits protein synthesis; it inactivates the 60S ribosomal subu
nto the cell of the A chain; B chains are also responsible for cell agglutination (lecti
C;Comment: This protein is cytotoxic and very poisonous to animals.
C;Superfamily: ricin; rRNA N-glycosidase homology
C;Keywords: duplication; glycoprotein; glycoprotein; glycosidase; hydrolase; lectin; RNA binding; seed
F;1-35/Domain: signal sequence #status predicted <SIG>
F;36-302/Product: ricin D chain A #status experimental <ACH>
F;36-302/Product: ricin D chain A #statu
                                        J. Biol. Chem. 260, 15682-15686, 1985
A; Title: The primary sequence of Ricinus communis agglutinin. A; Reference number: A24261; MUID:86059449; PMID:2999130
A; Accession: A24261
A; Molecule type: mRNA
A; Residues: 1-564 < ROB>
                                                                                                                                                                                                                                                                                                                                                                                                                                     agglutinin precursor - castor bean N;Contains: rRNA N·glycosidase (EC 3.2.2.2) C;Species: Ricinus communis (castor bean) C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999 C;Accession: A24261; A24210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proteins 10, 251-259, 1991
A; Title: Structure of ricin A-chain at 2.5 angstroms.
A; Reference number: A48239; MUID:91352004; PMID:1881881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 315-335,'N',337-342,'NH',345-362,364-383,'PS',386-399,'T',401,'D',403,'E',40527,'P',529-564,'W',566,'H',567-570,'LI',573-574,'F' <FUN>
A;Note: this paper, one of energy summarizes the experimental details for the determing R;Ready, M,P.; Kim, Y.; Robertus, J.D.

Proteins 10, 270-278, 1991

A;Title: Site-directed mutagenesis of ricin A-chain and implications for the mechanism of the site of the site of the site of the mechanism of the site of the 
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A;Cross-references: GB:M12089; NID:g169700; PIDN:AAA33869.1; PID:g169701
                                                                                                                                                                                                                                                                                                                                                                                            R; Roberts, L.M.; Lamb,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RLCSAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Contents: annotation; X-ray crystallography, 2.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: Structure of ricin B-chain at 2.5 angstrom resolution. A; Reference number: A48238; MUID:91352005; PMID:1881882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Rutenber, E.; Robertus, Proteins 10, 260-269, 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Contents:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           156 GNYDRLEQLAGNLRËNIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FOYIEGEMRTRIRYNRRS 233
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                                                                                                                                                                                                                                                                                                                                                                                       I.F.; Pappin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                            D.J.C.; Lord, J.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                               Comparison with ricin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   abrin-d precursor - Indian licorice (fragment)
N;Contains: rRNA N-glycosidase (EC 3.2.2.22)
C;Species: Abrus precatorius (Indian Licorice)
C;Date: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 01-Aug-1997
C;Accession: S32431; S34408
C;Superfamily: ricin; rRNA N-glycosidase homology C;Keywords: disulfide bond; duplication; glycoprotein; g F;1-251/Product: abrin-d chain A #status predicted <ACH>F;7-246/Domain: rRNA N-glycosidase homology <RNO>F;261-528/Product: abrin-d chain B #status predicted <BC
                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M98346
C;Comment: Abrin consists of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R:Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
J. Mol. Biol. 229, 263-267, 1993
A;Title: Primary structure of three distinct isoabrins determined A;Reference number: S32429; MUID:93132798; PMID:8421313
A;Accession: S32431
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                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-169, 'C', 171-320, 'L', 322-528 <HU2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Hung, C.; Lee, M.; Lee, T.; Lin, Submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-528 < HUN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: $34408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S32431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
                                                                                                                                                                                                                                                                               D;Comment: Abrin consists of an A chain, which inhibits protein synthesis by inactiva The A and B chains are linked by a single disulfide bond, which is essential for tox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Lin, J.

March 1993

cDNA sequencing.

predicted <BCH;

glycosidase; hydrolase;

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A; Accession: A24210
A; Accession: A24210
A; Accession: A24210
A; Molecule type: protein
C; Mole
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Biochim. Biophys. Acta 872, 277-285, 1986
A;Title: The complete amino acid sequence of the B-chain of the Ricinus communis aggl
A;Reference number: A24210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                               121 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 IFPKQYPIINETTADATVESYTNFIRAVRSHLTTGADVRHEIPVLPNRVGLPISQRFILV 84
                                                                                                                                                                                                                               GNYDRLEQL-GGLRENIELGTGPLEDAISALYYYSTCGTQIPTLARSFMYCIQMISEAAR 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 60
FOYIEGEMRTRIRYNRRS
                                                       FQYIEGEMRTRIRYNRRS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELSNHAELSVTLALDVTNAYVVGCRAGNSAYFFHPDNQEDAEAITHLFTDVQNSFTFAFG 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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91.9%;
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A;Cross-references: EMBL:X55667; NID:g16084; PIDN:CAA39202.1; PID:g16085
C;Comment: Abrin consists of an A chain, which inhibits protein synthesis by inactivating the A and B chains are linked by a single disulfide bond, which is essential for toxical C;Commently: ricin; rRNA N-g1ycosidase homology
C;Reywords: duplication; g1ycoprotein; g1ycosidase; hydrolase; lectin; pyroglutamic acid F;35-285/Product: abrin-c chain A *status predicted AACH>
F;41-280/Domain: rRNA N-g1ycosidase homology <RNG>
F;317-359,360-400,403-441,448-483,487-526.592-662/Region: 40-residue repeats F;317-359,360-400,403-441,448-483,487-526.592-662/Region: 40-residue repeats F;318-303,930/Binding site: substrate (Tyr, Tyr, Glu, Asn) *status predicted F;198,147,229,230/Binding site: substrate (Tyr, Tyr, Glu, Asn) *status predicted F;198,201/Active site: Glu, Arg *status predicted F;198,201/Active site: Glu, Arg *status predicted F;281-303,320-339.583-380,451-464,490-507/Disulfide bonds: *status predicted F;281-303,320-39,583-380,451-464,490-507/Disulfide bonds: *status predicted F;322,346/Binding site: N-acetylgalactosamine (Asp, Asn) *status predicted F;534,555/Binding site: N-acetylgalactosamine (Asp, Asn) *status predicted F;534,55
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A;Title: Preproabrin: genomic cloning, characterisation A;Reference number: S16022; MUID:91266957; PMID:2050149
A;Accession: S16022
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S16022
S16022
abrin-c precursor - Indian licorice
N;Contains: rRNA N-glycosidase (EC 3.2.2.2)
C;Species: Abrus precatorius (Indian licorice)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 20-Aug-1999
C;Accession: S16022
R;Wood, K.A.; Lord, J.M.; Wawrzynczak, E.J.; Piatak, M.
Eur. J. Biochem. 198, 723-732, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-562 < WOO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ρ
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                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 DLERWAHQTREEISLGLQALTHAIS----FLRSGASNDEEKARTLIVIIQMASEAARYRYI 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59 SERESIEVGIDVTNAYVVAYRAGSQSYFL---RDAPASASTYLFPGTQ-RYSLRFDGSYG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65
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                                                                                                                                                                                                                                                                                                                                                                                                Similarity
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SERESIEVGIDVTNAYVVAYRAGSQSYFL---RDAPASASTYLFPGTQ-RYSLRFDGSYG 148
                                                                               HAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYD 124
                                                                                                                                                                   QDQVIKFTTEGATSQSYKQFIEALRQRLTGG--LIHDIPVLPDPTTVEERNRYITVELSN
                                                                                                                                                                                                                                                  QYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSN 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGEMRTRIR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QDQVIKFTTEGATSQSYKQFIEALRQRLTGG--LIHDIPVLPDPTTVEERNRYITVELSN 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYI 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSN 64
                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                       34.7%; Score 353.5; 45.5%; Pred. No. 5.
                                                                                                                                                                                                                                                                                                                                               24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24; Mismatches
                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                      No. 5.3e-24; smatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Length 562;
                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and
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                                                                                                                                                                                                                                                                                                                                      Gaps
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C;Keywords: dissifide bond; duplication; glycoprotein; glycosidase; hydrolase; l; F;1-250/Product: abrin-b chain A *status predicted <ACH>F;7-245/Domain: rRNA N-glycosidase homology <RNG-F;260-527/Product: abrin-b chain B *status experimental <BCH>F;260-527/Product: abrin-b chain B *status experimental <BCH>F;260-784,325-365,368-406,413-448,452-491,494-527/Region: 40-residue repeats F;74,113,194,195/Binding site: substrate (Tyr. Tyr. Glu, Asn) *status predicted F;163,166/Active site: carbohydrate (Asn) (covalent) *status predicted F;260-268,285-304,328-345,416-429,455-472/Disulfide bonds: *status predicted F;267,311/Binding site: N-acetylgalactosamine (Asp, Asn) *status predicted F;267,311/Binding site: N-acetylgalactosamine (Asp, Asn) *status predicted F;499,520/Binding site: N-acetylgalactosamine (Asp, Asn) *status predicted F;
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J. Mol. Biol. 229, 263-567, 1993
A;Title: Primary structure of three distinct isoabrins determined by cDNA sequencing.
A;Reference number: S32429; MUID:93132798; PMID:8421313
A;Accession: S32430
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A; Residues: 260-281, 'D', 283-290, 'N', 292-349, 'PQ', 352-377, 'N', 379-425, 'M', 427, 'D', 429-
A; Experimental source: seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, A;Reference number: JC1398; MUID:93169023; PMID:7763422
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A; Residues: 1-527 <HUN>
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C;Date: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      abrin-b precursor - Indian licorice (fragment)
N;Contains: rRNA N-glycosidase (EC 3.2.2.22)
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171
                                                                                  185
                                                                                                                                                                                   115
                                                                                                                                                                                                                                                                125 RLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYI 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 RLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYI 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                               65 HAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 QYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSN 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
SYRVGVSIRTN 181
                                                                                  EGEMRTRIRYN 195
                                                                                                                                                                    DLERLARQTRQQIPLGLQALRHAISFL----QSGTDDQEIARTLIVIIQMASEAARYRFI 170
                                                                                                                                                                                                                                                                                                                                                             SDTESIEAGIDVSNAYVVAYRAGNRSYFL---RDAPTSASRYLFTGTQ-QYSLRFNGSYI 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QDQVIKFTTEGATSQSYKQFIEALRQRLTGG--LIHGIPVLPDPTTLQERNRYISVELSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EGEMRTRIR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DLERWAHQTREEISLGLQALTHAIS---FLRSGASNDEEKARTLIVIIQMASEAARYRYI 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 345; DB 2;
Pred. No. 2.9e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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rRNA N-glycosidase (EC 3.2.2.2) alpha-trichosanthin precursor [validated] - Mongolia N;Alternate names: alpha-TCS; type I ribosome-inactivating protein C;Species: Trichosanthes kirilowii (Mongolian snake-gourd)

(Mongolian snake-gourd)

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A; Contents: annotation; X-ray crystallography, 1.6 angstroms, with adenine, residues 24-R; Huang, 0; Liu, S; Tang, Y; Jin, S; Wang, Y.

submitted to the Brookhaven Protein Data Bank, July 1994

A; Reference number: A67092; DBB:IMRK

A; Contents: annotation; X-ray crystallography, 1.6 angstroms, with formycin, residues 24-R; Xiong, J.P.; Xia, Z.X; Wang, Y.

submitted to the Brookhaven Protein Data Bank, December 1994

A; Reference number: A67012; DBB:IMRK

A; Contents: annotation; X-ray crystallography, 1.7 angstroms, with NADPH, residues 24-R; Xiong, J.P.; Xia, Z.X; Wang, Y.

R; Xiong, J.P.; Xia, X.

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A; Molecule type: DNA
A; Residues: 1-233,'T',235-246,'M',248-289 <CHO>
A; Residues: 1-233,'T',235-246; MID:9170534; PIDN:AAA34206.1; PID:9170535
A; Cross-references: GB:J05434; NID:9170534; PIDN:AAA34206.1; PID:9170535
R; Zheng, H.G.; Wang, B.; Shao, P.Z.; Yang, X.R.
Acta Genet. Sin. 21; 42-51, 1994
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A;Title: Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a type I rib
A;Reference number: A36274; MUID:90256790; PMID:2341400
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A;Title: Scientific evaluation of Tian Hua Fen (THF): history, chemistry and application A;Reference number: JT0003
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A;Title: Primary amino acid sequence of alpha-trichosanthin and molecular models for
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A; Residues: 1-289 <SHA>
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A;Molecule type: protein
A;Residues: 24-56,'L',58-59,'I',61-71,'I',73-81,85-86,'L',88-92,'DAGLPRNAVL',93-142,'GL
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A; Residues: 1-72,'V',74-90,'S',92-233,'T',235-267,'D',269-289 <ZHE>
A; Cross-references: GB:S70176; NID:9547148; PIDN:AAB31048.1; PID:9547149
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R:Toyokawa, S.; Takeda, T.; Kato, Y.; Wakabayashi, K.; Ogihara, Y. Chem. Pharm. Bull. 39, 1244-1249, 1991
A;Title: The complete amino acid sequence of an abortifacient protein, karasurin. A;Reference number: JU0393; MUID:92005921; PMID:1914000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          karasurin - Mongolian snake-gourd
C;Species: Trichosanthes kirilowii (Mongolian snake-gourd)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 12-Apr-1995
C;Accession: JU0393; PS0163
                                                               R;Kondo, T.; Mizukami, H.; Takeda, T.; Ogihara, Y.
Biol. Pharm. Bull. 19, 1485-1489, 1996
A;Title: Amino acid sequences and ribosome-inactivating
A;Reference number: JCS032; MUID:97108848; PMID:8951169
A;Accession: JC5032
                                                                                                                                                                                                           karasurin-B - Trichosanthes kirilowii var. japonica
C;Species: Trichosanthes kirilowii var. japonica
C;Date: 27-Feb-1997 #sequence_revision 27-Feb-1997
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F;4-243/Domain: rRNA N-glycosidase homology <RNG>
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A; Molecule type: protein A: Residues: 1-247 < KON>
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                                             A;Status: preliminary
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A;Status: preliminary
A;Molecule type: protein
A;Residues: 22-270 <KON>
A;Residues: 22-270 <KON>
C;Comment: This protein is a ribosome-inactivating protein and exhibit cytotoxic, abortic;Comment: This protein belongs to type I ribosomal-inactivating proteins which catalytic;Comment: This protein belongs to type I ribosomal-inactivating proteins which catalytic;Comment: This protein belongs to type I ribosomal-inactivating proteins which catalytic;C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
F;22-270/Product: karasurin A #status predicted <MAA>
F;27-266/Domain: rRNA N-glycosidase homology <RNG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: DDBJ;AB000666; NID:g2329830; PIDN:BAA21786.1; PID:g2329831 R;Kondo, T.; Mizukami, H.; Takeda, T.; Ogihara, Y. Biol. Pharm. Bull. 19, 1485-1489, 1996 A;Title: Amino acid sequences and ribosome-inactivating activities of karasurin-B and A;Reference number: JC5032; MUID:97108848; PMID:8951169
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C;Species: Trichosanthes kirilowii var. japonica
C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 #text_change 19-Jul-2002
C;Accession: JC5606; JC5033
R;Mizukami, H.; Iida, K.; Kondo, T.; Ogihara, Y.
Biol. Pharm. Bull. 20, 711-713, 1997
A;Reference number: JC5606; MUID:97356562; PMID:9212998
A;Accession: JC5606
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                                                         188 MRTRI 192
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                                                                                                                          139 IAAGKIRENIPLGLPALDSAITTLFYYNAN-----SAASALMYLIQSTSEAARYKFIEQQ
                                                                                                                                                                                           128 QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 187
                                                                                                                                                                                                                                                                82 TISVAIDVTNVYVMGYRAGDTSYFF---NEASATEAAKYVFKDAKRKVTLPYSGNYERLQ
                                                                                                                                                                                                                                                                                                                                 69 SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 127
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pred. No. 4.6e-23;
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A;Cross-references: GB:M98344; NID:g166294; PIDN:AAA32624.1; PID:g166295 A;Note: the coding region for the sequence shown is preceded by an ATG cc A;Note: residues 1-8 were derived from the synthesized primer R;Funatsu, G:; Taguchi, Y:; Kamenosono, M.; Yanaka, M. Agric. Biol. Chem. 52, 1095-1097, 1988
                                                                                                                                                                                                                                                                                                                                                                abrin-a precursor - Indian licorice (fragment)
N;Contains: IRNA N-glycosidase (EC 3.2.2.22)
C;Species: Abrus precatorius (Indian licorice)
C;Date: 31-Dec-1993 #sequence_revision 01-Aug-1997 #text_change 16-Jul-1999
C;Accession: S32429; JT0202; A39761; JC1398; S14472; S24133; S74110; S74111
R;Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
J. Mol. Biol. 229, 263-267, 1993
A;Title: Primary structure of three distinct isoabrins determined by cDNA s
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                                                                                                                                                                                   A; Molecule type: mRNA
A; Residues: 'E', 2-528 <HUN>
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N;Contains: rRNA N-91ycosidase (EC 3.2.2.22)
C;Species: Abrus precatorius (Indian licorice)
C;Date: 21-Feb-1992 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
C;Accession: C39761; S14471
                                                                                                                                                                                                                                                        A; Status: nucleic acid sequence not shown
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J. Biol. Chem. 266, 6848-6852, 1991
A;Title: Direct molecular cloning and expression of two
A;Reference number: A39761; MUID:91201329; PMID:2016300
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A; Residues: 'M', 1-251 <EV2>
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A; Residues: 1-251 <EVE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GVSIR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RTRIR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WAHQTREQISLGLQALTHAIS---FLRSGASNDEEKARTLIVIIQMASEAARYRYISNRV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEM 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIEVGIDVTNAYVVAYRAGSQSYFL---RDAPASASTYLFTGTQ-RYSLRFDGSYGDLER 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQ 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IKFSTEGATSQSYKQFIEALRERLRGG--LIHDIPVLRDPTTVEERNRYITVELSNSERE 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.0%; Score 336.5;
44.9%; Pred. No. 6.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24; Mismatches
                                                                                                                                                                                                                                                                                                                                         PMID:8421313
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                                                                                                                                                                                                                                                                                                                                                                    by cDNA sequencing.
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                                                                                                               codon
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A;Note: residues 1-8 were derived from the synthesized primer R;Kimura, M.; Sumizawa, T.; Funatsu, G. Biotechnol. Biochem. 57, 166-169, 1993
Biosci. Biotechnol. Biochem. 57, 166-169, 1993
A;Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, A;Reference number: JC1398; MUID:93169023; PMID:7763422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, we have R;Evensen, G.; Mathlesen, A.; Sundan, A. J. Biol. Chem. 266, 6848-6852, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: The complete amino acid sequence of the A-chain of abrin-a, a toxic protein fro A; Reference number: JT0202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C:Keywords: duplication: glycoprotein: glycosidase; hydrolase; lectin; pyroglutamic aci. F:1-251/Product: abrin-a chain A *status experimental <ACH>
F:7-246/Domain: rRNA N-glycosidase homology CRNG>
F:26-528/Product: abrin-a chain B *status experimental <BCH>
F:283-325.326-366,369-407,414-449,433-492,495-528/Region: 40-residue repeats
F:1/Modified site: pyrrolidone carboxylic acid (Gln) *status experimental
F:74,113,195,196/Binding site: substrate (TTy, Tyr, Glu, Asn) *status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: JT0202
                                                                                                                                                                                                                                                                                              F;164,167/Active site: Glu, Arg #status predicted F;247-269,286-305,329-346,417-430,456-473/Disulfide bonds: #status predicted F;248-312/Binding site: wacetylgalactosamine (Asp. Asn) #status predicted F;361,401/Binding site: carbohydrate (Asn) (covalent) #status experimental
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A;Experiment: Abrin-a is more toxic than ricin. The toxin consists of an A chain, which inle taining receptors on the cell surface. The A and B chains are linked by a single disulfitation of the cell surface to the consists of an A chain, which in the content of the constant of the content o
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A;Molecule type: 262-297, 'Y',299-426, 'L',428-466, 'P',468-482, 'L',484-528 <CHE>
A;Residues: 262-297, 'Y',299-426, 'L', Liaw, Y.C.; Chen, J.K.; Lin, J.Y.
R;Lin, S.H.; Chow, L.P.; Chen, Y.L.; Liaw, Y.C.; Chen, J.K.; Lin, J.Y.
Eur. J. Biochem. 240, 564-569, 1996
A;Title: Probing the domain structure of abrin-a by tryptic digestion.
A;Reference number: S74110; MUID:97008945; PMID:8856055
A;Accession: S74110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, October 1990
A; Description: Direct molecular cloning of two distinct abrin A-chains.
A; Reference number: $14471
A; Accession: $14472
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A; Residues: 261-347, 'T', 349-351, 'A', 353-357, 'L', 359-528 <KIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Cross-references: GB:X54872
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A; Residues: 'E', 2-251 <EVE>
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                                                                                                                                                                                                                                        F;361,401/Binding site: carbohydrate (Asn) (covalent) *status experimental F;500,521/Binding site: N-acetylgalactosamine (Asp, Asn) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein
A; Residues: 262-276, 'X', 278-280; 329-348; 369-388; 399-418 <LIW>
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A; Residues: 89-108; 154-172 <LIN>
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A; Residues: 'ME', 2-251 <EV2>
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                                           Conservative
                           32.3%; Score 329.5; DB 1
42.8%; Pred. No. 7.2e-22;
tive 28; Mismatches 66
                                                                                                                                       DB 1; Length 528;
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                                                                                                      C; Superfamily: rRNA N-glycosidase; F; 5-246/Domain: rRNA N-glycosidase
                                                                                                                                                                                                        A; Molecule type: protein A; Residues: 1-250 <ISL>
                                                                                                                                                                                                                                                                                                                                                                                                                R;ISlam, M.R.; Hirayama, H.; Funatsu, G. Agric. Biol. Chem. 55, 229-238, 1991
A;Title: Complete amino acid sequence of luffin-b, a ribosome-inactivating protein A;Reference number: JN0108; MUID:91248488; PMID:1368666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Luffa cylindrica (smooth loofah)
C;Date: 04-Sep-1998 #sequence_revision 04-S
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Query Match
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29.5%; Score 300.5;

DB

Length 250

homology

<RNG>

rRNA N-glycosidase homology

04-Sep-1998 #text\_change 07-May-1999

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A;Cross-references: EMBL:X62372; NID:g19149; PIDN:CAA44230.1; PID:g19150
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
F;26-264/Domain: rRNA N-glycosidase homology <RNG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Kataoka, J.; Habuka, N.; Miyano, M.; Masuta, C.; Koiwai, A. Plant Mol. Biol. 19, 887-889, 1992
A;Title: Nucleotide sequence of cDNA encoding beta-luffin, another ribosome-inactivat A;Reference number: S23519; MUID:92353400; PMID:1643290
A;Accession: S23519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   beta-luffin - smooth loofah (Speckes: Luffa cylindrica (smooth loofah) (Speckes: Luffa cylindrica (smooth loofah) (C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 20-Aug-1999 (C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 20-Aug-1999 (C;Accession: S23519; S23113
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A; Residues: 1-278 < KAT>
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                                                               189 RTRIRYN 195
                                                                                                                          187 EMRTRIR 193
193 IERIPKN 199
                                                                                                                                                                                             129 LAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEM 188
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                                                                                                                                                                                                                                                               81 AITMAIDVTNVYIMGYLVNSTSYFF---NESDAKLASQYVFKGSTIVTLPYSGNYERLQN 137
                                                                                                                                                                                                                                                                                                                              69 SYTLALDYTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQ 128
                                                                                                                                                                                                                                                                                                                                                                                                 24 VSFSLSGADSKSYSKFITALRKALPSKEKVSNIPLLLPSASGA----SRYILMQLSNYDAK 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 IKFSTEGATSQSYKQFIEALRERLRGG--LIHDIPVLPDPTTLQERNRYITVELSNSDTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ERWAHQSRQQIPLGLQALTHGIS---FFRSGGNDNEEKARTLIVIIQMVAEAARFRYISN 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30.1%; Score 307.5; 35.8%; Pred. No. 3e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 3e-2
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3e-20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64;
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mistletoe lectin I A chain - Viscum album (fragment)
C;Species: Viscum album
C;Species: Viscum album
C;Date: 03-Jul-1998 #sequence_revision 10-Jul-1998 #text_change 26-Aug-1999
C;Accession: PD0018
R;Bschenburg, S.; Krauspenhaar, R.; Mikhailov, A.; Stoeva, S.; Betzel, C.; Voelter, W.
Biochem. Biophys. Res. Commun. 247, 367-372, 1998
A;Title: Primary structure and molecular modeling of mistletoe lectin I from Viscum albu
A;Reference number: PD0018; MUID:98308123; PMID:9642133
                                                                                                                                                                      RESULT 15
PD0018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: protein
A;Residues: 29-39;309-319 <VA2>
C;Superfamily: ricin; rRNA N-glycosidase homology
F;37-283/Domain: rRNA N-glycosidase homology <RNG>
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A;Molecule type: mRNA
A;Residues: 1-570 <VAN>
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                                                                                                                                                                                                                                                                                       178 AARFQYIEGEMRTRI 192
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                                                                                                                                                                                                                                                                                                                                                                                                     87 PLTNPSGDTVTLAIDVVNLYVVAFSSNGKSYFFSGSTAVQRD-----NLFVDT-TQEELN 140
                                                                                                                                                                                                                                                                                                                                                                                                                                           61 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDN--QEDAEAITHLFTDVQNRYTFA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29 VTPPVYPSVSFNLTGA--DTYEPFLRALQEKVILGNHTAFDLPVLNPESQVSDSNRFVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 AITMAIDVTNVYIMGYLVNSTSYF---ANESDAKLASQYVFKGSTLVTIPYSGNYERLQN 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 IFPKQYPIINETTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIIGIQMISEAARFQYIEGEM 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQ 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VSFSLSGADSKSYSKFITALRKALPSKEKVSNIPLLLPSASGA---SRYILMQLSNYDAK 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL
                                                                                                                                                                                                                                                   AARFRYIELRIRTSI 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RTRIRYN 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGKIREKIPLGFRALDSALTSIFHYDS-----TAAAAAFLVILQTTAEASRFKYIEGQI 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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o. wismatches 64;
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A;Molecule type: protein
A;Residues: 1-254 <ESC>
C;Superfamily: ricin; rRNA N-glycosidase homology
E;7-246/Domain: rRNA N-glycosidase homology <RNG>
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                                                                                                                                                        67 TAAIDVTNAYVVAYQAGDQSYFLR-DAPRGAE--THLFTGT-TRSSLPFNGSYPDLERYA 122
                                                                                                                                                                            71 TLALDYTNAYYVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLA 130
                                                                                                                                                                                                                                                                       13 TAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPIN--QRFILVELSNHAELSV 70
                                                                                                                                                                                                                                                                                                              81;
                                                                                                                                                                                                                                   9 THQTTGEEYFRFITLLRDYVSSGS-FSNEIPLL-RQSTIPVSDAQRFVLVELTNQGQDSV
YINSGASFLPDVYMLELETSWGQQSTQVQHS 209
                                                                           GH-RDQIPLGIDQLIQSVTALRF---PGGSTRTQARSILILIQMISEAARFNPILWRYRQ 178
                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                28.0%; Score 286; DB 2; 38.4%; Pred. No. 2.4e-18;
                                        -----GEMRTRIRYN 195
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Search completed: September 16, Job time: 13.8414 secs 2003, 11:50:33

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Minimum DB
Maximum DB
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                 98765492
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Gapop 10.0 , Gapext 0.5
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Ricin A chain. Un Ricin A-chain (RTA Ricin A-chain ribo Ricin A-chain RIP. Ricin A. Escheric Sequence of Ricinum Ricin A encoded by Anti-cataract immu Ricin D. Ricinus
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342 33.5 342 33.5	33.	42 33.	2 33.	33.	33.	•	42 33.	33.	33.	2 33.	76.	96.5	.5 91.	30.5 91.	96.	97.	98.	99.	99.		99.	99.	1013 99.3	99.	99.		99.	100.		0 100.	0 100.	20 100.	0	1020 100.0
289 289 1																																		
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richosant cucumber				Ti.	· •3	Trichosanthin (a r	$\mathbf{\sigma}$		quen	Trichosanthin anti	gglu	uence of I	nunis	r oil	P	A chai	gene prod	nce of	acid se	ρI	O	cin.	of R		hetic	bean	ence of p	tor bean	bean prepr	s comm	_	ean	ce of Ricin	Modified castor be

## ALIGNMENTS

RESULT 1 AAR37290 25-MAR-2003 09-JAN-2003 13-SEP-1993 04-NOV-1991; 19-JUN-1992; Type II ribosome-inactivating protein; type II RIP; gelonin; momordin; immunoconjugate; autoimmune disease; cell killing; toxin. WPI; 1993-167617/20 Berhard SL, (XOMA ) XOMA CORP. 04-NOV-1992; 13-MAY-1993. WO9309130-A1 Unidentified Ricin A chain. AAR37290; AAR37290 standard; protein; 267 Better MD, (updated)
(updated)
(first entry) 91US-0787567 92US-0901707 92WO-US09487 Carroll Å SF, Lane JA, Lei

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disulphide bonding at an amino acid position corresp. to a position not naturally available for bonding; the cys residue is located in the C-terminal region of the analogue between a position corresp. to amino acid 251 and the C-terminus of ricin A chain. The analogues are pref. joined via a disulphide linkage to a molecule which specifically binds to a target cell, e.g. an antibody fragment. (Updated on 09-JAN-2003 to add missing OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Analogues of type I ribosome inactivating protein - useful as cytotoxic agents, immuno toxins for treating auto immune diseases, cancer, graft versus host disease and selective cell killing in-vivo
 Polynucleotide(s) encoding
                     WPI; 1995-006804/01.
                                                                                                                                                                                       Ricin A chain; RTA; ribosome-inactivating proteins; RIPs; cytotoxic therapeutic agents; autoimmune disease; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention covers analogues of Type I RIPs. Ricin is a Type II RIP whose A chain is homologous to plant type I RIPs. The analogues of the invention have a cysteine available for intermolecular
                                         Better
                                                          (XOMA ) XOMA CORP
                                                                             12-MAY-1993;
                                                                                                 12-MAY-1994;
                                                                                                                                        WO9426910-A1.
                                                                                                                                                           Ricinus communis.
                                                                                                                                                                              graft-versus-host disease.
                                                                                                                                                                                                                     Ricin A-chain (RTA).
                                                                                                                                                                                                                                        25-MAR-2003
27-JUL-1995
                                                                                                                                                                                                                                                                    AAR63902;
                                                                                                                                                                                                                                                                                       AAR63902 standard; protein;
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                                                                                                                    24-NOV-1994.
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                                                                                                                                                                                                                                                                                                                                       FQYIEGEMRTRIRYNRRS 198
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                                        Carroll
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(first entry)
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                                                                                                 94WO-US05348
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                                        Studnicka
 type I ribosome-inactivating proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 1020; DB 14;
Pred. No. 4.9e-100;
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                                        ΩM,
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09-DEC-1992;
11-JUN-1990;
26-JAN-1995;
07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ricin A-chain; Abrin-A A-chain; Saporin; SLT-1; Luffin A; MAP; Ricinus communis agglutinin; Momordin; PAP-S; Luffin-B; Dianthin 30; therapeutic toxin; tumour cell targeted; protein synthesis inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ricin A-chain ribosome inhibitory protein inactive precursor.

    which are suitable for use as components of cytotoxic
therapeutic agents.

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                                                                                                                                                                                                                                                          08-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maize; proRIP; ribosome inactivating protein; alpha; beta subunit; internal linker; Barley Translation Inhibitor; Trichosanthin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW25136 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Fig 1; 221pp; English.
                                                                                                                                                                                                                                                                                                                   US5646026-A
                                                                                                                                                                                                                                                                                                                                                                                                                                human immunodeficiency virus; acquired immune deficiency syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                              post-translational modification; cancer; neoplasia; HIV: AIDS;
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DOWELANCO.
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(first entry)
                                                                                 92US-0987927.
90US-0535636.
95US-0378761.
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Pred. No. 4.9e-100;
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RESULT 4
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AAW
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DT 26-5
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DE Ricl
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FI KEY
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         maize RIP, Trichosanthin, Ricin A-chain, Abrin-A A-chain and Saporin. The RIPs can be used in the construction of therapeutic toxins targeted to specific cells such as tumour cells via the attachment of a targeting polypeptide, e.g. a monoclonal antibody. A further use is in HIV therapy (see US4869903). There is interest in expressing RIP recombinantly in host eukaryotic cells, because of the capacity to provide correct post-translational processing. However, RIPs effectively inhibit protein synthesis in eukaryotic cells resulting in cell death. Since the inactive RIP proteins are not cytotoxic to eukaryotic cells, they can be recombinantly expressed in such cells and then converted to active RIP proteins.
                                                                             pro-Ribosome Inactivating Protein; proRIP; peptide linker; cancer; inactivation; eukaryotic ribosome; alpha fragment; beta fragment; inhibitor; protein synthesis; N-glycosidase; glycosidic bond; liverat; ribosomal 28S RNA; cellular proliferation; HIV-infected T cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW25136 represents a Ricin A-chain ribosome inhibitory protein (RIP) which was engineered to contain a selectively removable internal peptide linker sequence separating the alpha and beta units of the RIP. When separated the two units regain activity and are capable of inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding pro-ribosome inactivating proteins - precursors of ribosome inactivating proteins; can eukaryotic cells without causing cell death
                                                     Ricinus
                                                                                                                                                                                                   25-MAR-2003
26-SEP-1997
                                                                                                                                                                                                                                                     AAW21699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eukaryotic ribosomes and hence preventing protein production. Many different RIPs may be produced with an internal linker including
                                                                                                                                                                    Ricin A-chain RIP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   converted to active RIP proteins. ated on 25-MAR-2003 to correct PF field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  290 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                  (updated)
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     Location/Qualifiers 152..162
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Pred. No. 5.4e-100;
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                                                                                                   liver;
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequences given in AAW21698-710 represent Ribosome Inactivating CP Proteins (RIP's), which may be used in the construction of the protein of the invention. The proRIP has a selectively removable, internal peptide linker. The precursor sequence is incapable of inactivating eukaryotic ribosomes, but can be converted by removal of the linker into a protein having alpha and beta fragments and being capable of inactivating eukaryotic ribosomes. RIPs are potent substituted inhibitors of eukaryotic protein synthesis. They possess a highly specific N-glycosidase activity which cleaves the glycosidic bond of adenine 4324 of rat liver ribosomal 28S RNA. RIP's selectively inhibit cellular proliferation of cells, e.g. cancer cells and HIV-infected T cells. The inactive proRIP proteins make it possible to provide protein synthesis inhibitors with uses in practical and improved ways not before possible. The RIP can be used to make cytotoxic conjugates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-DEC-1992;
11-JUN-1990;
26-JAN-1995;
                                  09-APR-1991
                                                                                                AAP70097 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inactive precursor of maize ribosome-inactivating protein - also chimeric ribosome-inactivating protein precursors containing internal linker sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
                                                                                                                                                                                                                                                                                                                                 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Column
                                                                                                                                                                                                              FOYIEGEMRTRIRYNRRS 198
                                                                                                                                                                               FQYIEGEMRTRIRYNRRS 222
                                                                                                                                                                                                                                                GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
                                                                                                                                                                                                                                                                                                               ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                                                                                                                                                                                                                                                                                                                                 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92US-0987927.
90US-0535636.
95US-0378761.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95US-0378761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91-94; 121pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Position of possible insertion of internal
peptide linker sequence"
                                                                                              protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Walsh TA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1020; DB 18; Pred. No. 5.4e-100;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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RESULT 6
RAP708 ID AAP7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 198; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                 25-MAR-2003
18-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  using Met-aminopeptidase from E.coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig. 4; 20pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-terminal methionine free proteins prodn. - by using host transformed with vector to express a methionine-amino-peptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Benbassat A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-MAY-1986;
20-SEP-1985;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-APR-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ricin A; Met-aminopeptidase
      Region
                                                                                                                                             plant toxin.
                                                                                                                                                                                                                          Sequence of Ricinus communis castor beans ricin toxin (RT or ricin)
                                                                                                                                                                                                                                                                                                                                                                 AAP70838 standard; protein; 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ricin A may be produced in a form which lacks an N-terminal Met
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAN70152
                                           Region
                                                                                                     Ricinus communis
                                                                                                                                                             Lectin; toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CETU ) CETUS CORP
                                                                                                                                                                                                     protein encoded by pRA123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1987-110172/16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 ELSNHAELSYTLALDYTNAYYYGYRAGNSAYFFHPDNQEDAEAITHLFTDYQNRYTFAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FQYIEGEMRTRIRYNRRS 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FQYIEGEMRTRIRYNRRS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   332 AA;
                                                                                                                                                                                                                                                                 (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bauer KA,
                                                                                                                                                                protein; cytotoxic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     86US-0860330
85US-0778414
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    /note="Leader"
33..302
                                           Location/Qualifiers
1..32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1020; DB 8;
Pred. No. 6.5e-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                   A
                                                                                                                                                                cytostatic; castor bean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chang SY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 332;
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                                                                                                                                               RESULT 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CC (AAN70525), putative ricin E (AAN70526) and RCA (AAN70524) in precursor CC (AAN70525), putative ricin E (AAN70525) and RCA (AAN70524) in precursor CC (Form were obtd. using messenger RNA to obtain a cDNA library, and CC then probing the library to retrieve the desired cDNA library, and CC (AAN70520) and RCA (AAN70514. Figure 4 (see CC AAN70520, AAN70521, AAN70522) shows the nucleotide sequences of three CC plasmids contg. cDNA inserts obtd. by probing a cDNA library for CC sequences encoding ricin B using the probe in AAN70517. The cDNA CC inserts can be placed into expression vectors. Site-directed CC mutagenesis may be used to place an AFG start codon and a HindIII CC site at the beginning of the mature protein (see AAN70518). The CC coding sequences of the inserts can be ligated into expression CC (AAN70523) and suitable retroregulators.

CC (AAN70523) and suitable retroregulators.

CC (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                AAP95639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New non-glycosylated ricin precursor and toxin etc. -
by recombinant DNA procedures with specific isolation
purer and soluble prods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1987-265177/38
N-PSDB; AAN70519.
        25-MAR-2003
31-OCT-2002
                                                                                                     AAP95639 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CETU ) CETUS CORP. (CHIR ) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-MAR-1986;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 1; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-SEP-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                              181 FQYIEGEMRTRIRYNRRS 198
                                                                                                                                                                                                                                                                                      156 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
                                                                                                                                                                                                                                                                                                       121 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 180
                                                                                                                                                                                                           216 FQYIEGEMRTRIRYNRRS 233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                              332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
      (updated)
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315..332
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                                                                                                         332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 332;
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Best Local
                                                                                                                                                                                   Matches
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08-FEB-1984;
09-FEB-1984;
07-SEP-1984;
20-SEP-1984;
                                                                                                                                                                                                                                                                        (Updated
(Updated
(Updated
(Updated
                                                                                                                                                                                                                                                                                                                                                  Plasmid RA123 (ATCC No. 39799) carries the entire coding sequence for ricin A, as well as codons for 12 AAs joining the A to the B chain. Following modification for ease of manipulation the plasmid was used to construct expression vectors which express the conjugates in
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant vectors expressing ricin chains or diphtheria toxin prodn. of new immunotoxin conjugates with monoclonal antibodies, high cell specificity and good extracellular stability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI;
                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 14; 54pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Piatak MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gelfand D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CETU ) CETUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JAN-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ricinus
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                                                                                                                                                                                                                                                                                                                                        host cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1989-286959/40.
DB; AAN91281.
 156
            121 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
                                                         96
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                                                                                                                                                                                                                                                                        d on 31-OCT-2002 1
d on 25-MAR-2003 1
d on 25-MAR-2003 1
d on 25-MAR-2003 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      encoded
                                                                                                                                                                                                Similarity
                                                      GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
                                                                                                                                                                                                                                             332
                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lawyer FC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84US-0578121.
84US-0578122.
84US-0648759.
84US-0653515.
                                                                                                                                                                                                                                             Ą,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84US-0578115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89EP-0201162.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     by insert from plasmid pRA123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label=linker
315..332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303..314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= leader sequence 36..302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label=B-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label=A-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                                                                        to add missing OS field.)
to correct PF field.)
to correct PR field.)
to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Horn
                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ر.
و
                                                                                                                                                                                              Score 1020; DB 10;
Pred. No. 6.5e-100;
                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Greenfield L,
                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nitecki D,
                                                                                                                                                                                Indels
                                                                                                                                                                                                             Length
                                                                                                                                                                                                              332;
                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kaplan
                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            having
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ö
                            180
                                                                                      120
                                                                                                                     95
                                                         155
 215
                                                                                                                                                                                0,
                                                        RESULT 8
ANAR70827
ID ANAR70827
XX ANAR70827
XX ANAR70827
XX ANAR70827
XX Inmu
KW Inmu
FT Doma
FT Pep
FT Ooma
FT Pep
FT P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
 198;
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Qy
           Query Match
Best Local S
                                                                                                                   The immunotoxin given in AAR70827 comprises the heavy and light chain variable regions of anti-lens epithelium IgG3 MAb 4197X linked to ricin-A and a hexa-histidine tag. The DNA construct encoding the
                                                                                                                                                                                                             New single chain immuno:toxin - binds specifically to epithelial cells, for inhibiting development of sec. cataracts after extra:capsular cataract extraction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunotoxin; heavy chain; light chain; variable region; antibody;
ricin-A; cytostatic; cataract; lens opacification; epithelial cell;
pHB19; 4197X; monoclonal antibody; MAb.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAR-2003
31-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR70827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR70827
                                                          Sequence
                                                                                                                                                                                Disclosure; Fig.4; 68pp;
                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                          Gould RM,
                                                                                                                                                                                                                                                                                                                                                                                       02-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9503828-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anti-cataract
                                                                                       (Updated
                                                                                                         immunotoxin was expressed from pHB19 in E. coli.
                                                                                                                                                                                                                                                                                                                                                         (HOUS-) HOUSTON BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                             1995-082036/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
              Similarity
                                                                                                                                                                                                                                                                            AAQ85386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FQYIEGEMRTRIRYNRRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                                         on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FQYIEGEMRTRIRYNRRS
                                                                                                                                                                                                                                                                                                                          Kelleher
                                                          554
                                                                                         25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunotoxin
                                                          ΑĄ;
                                                                                                                                                                                                                                                                                                                                                                                       93US-0101329
                                                                                                                                                                                                                                                                                                                                                                                                                     94WO-US07919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "MAb 4197X
148..166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                549..554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note- "hexa-histidine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= LIGHT
/note= "MAb 419X light chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= RICIN-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label- LINKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= HEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "phoA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                          PJ,
           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sig_peptide
                                                                                                                                                                                  English.
                                                                                                                                                                                                                                                                                                                          Wallace TL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  signal
            Score 1020;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    heavy chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence"
                                                                                                                                                                                                                                                                                                                           Wood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tail"
              1.3e-99;
                             DB 16;
 0
                           Length
                              554;
0;
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Conservative

Mismatches

Indels

Gaps

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RESULT 9
AAP90079
ID AAP90079
XX AAP9
AC AAP9
XX AAP9
XX AAP9
XX AAP9
XX Rici
XX Rici
XX Rici
XX WO89
XX WO89
XX WO89
XX GEN
XX GEN
XX GEN
XX WPI Brow
XX WPI Brow
XX GEN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
                                                                                                                                                                            Query Match
Best Local Simi
Matches 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qy
                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                       of DNA from Ricinu communis, Zanibariensis variety. Patent discloses many modifications of ricin in which the lectin binding function of the B chain is diminished or removed, and conjugation to toxins to eliminate cell binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Modified ricin molecules and toxin conjugates - in which the lectin binding function of the B chain is removed or diminished to reduce cell binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; fig 1; 51pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ricin D; Ricinus communis; caster beans; Zanibariensis variety; modified; lectin binding removed; reduced cell binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ricin D (see corresp. AAN90068) found on the EcoRI-HindIII fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1989-178366/24.
N-PSDB; AAN90068.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-NOV-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-NOV-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ricinus communis (caster beans)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-2003
01-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP90079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAP90079 standard; protein; 562 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GEMY ) GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W08904839-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ricin D
                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EĽ,
                                                                           36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ELSNHAELSVTLALDVTNAVVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                                              IFPKQYPIINFTTAGATYQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 60
                                                                                                                                                                                                                                                                                                                                           on 25-MAR-2003
on 25-MAR-2003
                ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
                                                                  IFPKQYPIINETTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FQYIEGEMRTRIRYNRRS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FQYIEGEMRTRIRYNRRS 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                                                                                                                                                                                                                                         562 AA;
                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87US-0124735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88WO-US04238
                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                        to correct PA field.)
to correct PI field.)
                                                                                                                                                                               0
                                                                                                                                                                                                  Score 1020; DB 10 Pred. No. 1.3e-99;
                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                 DB 10;
                                                                                                                                                                               0
                                                                                                                                                                               Indels
                                                                                                                                                                                                                           Length 562;
                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120
                                                                     95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      337
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AAG78304
ID AAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Вр
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
                                      Example 1; Page 59-63; 66pp; English
                                                                      Novel composition comprising toxin e.g., useful for treating viral infections suc
                                                                                                                 WPI; 2001-581908/65
                                                                                                                                                                               16-FEB-2000; 2000US-0182759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric -
Chimeric -
                                                             virus infection.
                                                                                                      N-PSDB; AAI64145
                                                                                                                                                                                                                        23-AUG-2001.
                                                                                                                                                                                                                                             WO200160393-A1
                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                          Cleavage-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Castor bean plant; preproricin; ricin; A chain; B chain; human immunodeficiency virus infection; HIV; toxin; antiviral agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG78304 standard; Protein; 565 AA.
                                                                                                                                       Keener WK, Ward TE;
                                                                                                                                                                                                   15-FEB-2001; 2001WO-US05282
                                                                                                                                                                                                                                                                                                                                                             Protein
                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAG78304;
                                                                                                                                                          (BECH-) BECHTEL BWXT IDAHO LLC
                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          retroviral infection; anti-HIV; virucide; viral protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified castor bean preproricin (SEQ ID 10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FOYIEGEMRTRIRYNRRS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FOYIEGEMRTRIRYNRRS 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immunodeficiency virus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ricinus communis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                     /label= HIV_protease_cleavage_site
304..565
                                                                                                                                                                                                                                                                                                          296.
                                                                                                                                                                                                                                                                                                                               292..303
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                /note= "Galactose/N-acetylgalactosamine-binding lectin"
                                                                                                                                                                                                                                                                            /label=
                                                                                                                                                                                                                                                                                                          /label= Linker_peptide
296..297
                                                                                                                                                                                                                                                                                                                                                                                                               /label= Proricin
                                                                                                                                                                                                                                                                                                                                      /note= "N-glycosidase"
                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Signal_peptide
                                                                                                                                                                                                                                                                                                                                                   'label= Ricin_A_chain
                                                                                                                                                                                                                                                                                                                                                                                "Proricin consists of the ricin A chain, a linker peptide, and the ricin B chain. Proricin is proteolytically cleaved between the A chain and
                                                                                                                                                                                                                                                                            Ricin_B_chain
                                                                                                                                                                                                                                                                                                                                                                      the linker to yield mature ricin"
                                                                       such
                                                                      ricin based antiviral compound has human immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180
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The sequence relates to the amino acid sequence of a modified preproricin protein encoded by AAI64145. The invention relates to a novel toxin (e.g. ricin) based antiviral agent which is toxic to virus-infected

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         virucide activities. The agent is able to enter all HIV susceptible cells, and not just cells known to act as host cells for the virus. The antiviral agent remains inert in a cell unless the cell is infected with the HIV virus, where the viral protease activates it. Ricin's mechanism of action is through inactivation of cellular ribosomes and enhancement of binding of the antiviral agent to galactose residues on cell surfaces, and its cellular internalisation. The invention is useful infections, especially retroviral infections. The antiviral agent is activated in viral particles or early-stage infected cells, killing the viral genome into the host genome thereby preventing the integration of the viral genome into the host genome thereby preventing the latency/rebound
 (CETU ) CETUS CORP.
                                     07-MAR-1986;
                                                           13-NOV-1986;
                                                                                                                                               Region
                                                                                                                                                                                                                                                                                     Sequence of Ricinus communis (castor bean) Ricin toxin (RT or ricin) E precursor encoded by pRT38.
                                                                                                                                                                                                                                                                                                                             25-MAR-2003
21-MAY-1991
                                                                                                                                                                    Region
                                                                                                                                                                                                                                 Ricinus communis
                                                                                                                                                                                                                                                                  Lectin; toxin
                                                                                                                                                                                                                                                                                                                                                                                       AAP70326 standard; Protein; 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                        toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         but non-toxic to uninfected cells. The invention has anti-HIV and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FQYIEGEMRTRIRYNRRS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FOYIEGEMRTRIRYNRRS 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              565 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                           (updated)
(first entry)
                                                                                                                                                                                                                                                               protein; cytotoxic; cytostatic; castor bean;
                                    86US-0837583
                                                           86EP-0308877.
                                                                                                                                           /note= "A-chain"
315..576
                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                               'note= "leader"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                 "B-chain'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1020; DB 22
Pred. No. 1.3e-99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The full length sequences encoding ricin A (AAN70520), ricin D C (AAN70525) putative ricin E (AAN70526) and RCA (AAN70524) in precursor CC form were obtained, using the messenger RNA to obtain a cDNA library and CC then probing the library to retrieve the desired cDNA inserts. The CC (Library was probed using the 35-mer given in AAN70514. Figure 4 (see CC AAN70520, AAN70521, AAN70522), shows the nucleotide sequences of three CC (Library was probed using the 35-mer given in AAN70517. The cDNA inserts obtained by probing a cDNA library CC for sequences encoding ricin B using the probe in AAN70517. The cDNA inserts can be placed into expression vectors. Site-directed mutagenesis may be used to place an Arg start codon and a Hindill CC site at the beginning of the mature protein, (see AAN70518). The CC coding sequences of the inserts can be ligated into expression CC (AAN70523) and suitable retroregulators.

CC (AAN70523) and suitable retroregulators.

CC (Updated on 25-MAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                            Ricin; cytotoxin; hybrid protein; cell delivery; cell binding ligand; translocation domain; diphtheria toxin interleukin-2; T-cell lymphoma; organ rejection; therapy.
                                                                                                                                                                                                  Castorbean ricin
                                                                                                                                                                                                                                 25-MAR-2003
27-MAR-1998
                                                                                                                                                                                                                                                                                   AAW25787;
                                                                                                  Ricinus
                                                                                                                                                                                                                                                                                                                   AAW25787 standard; Protein; 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 14(1-2); 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New non-glycosylated ricin precursor and toxin etc. - are prepd
by recombinant DNA procedures with specific isolation steps for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Piatak M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                   216
                                                                                                                                                                                                                                                                                                                                                                                                                                181 FQYIEGEMRTRIRYNRRS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIIGIQMISEAAR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1987-265177/38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and soluble prods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IFPKQYPIINFTTAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV 60
                                                                                                                                                                                                                                                                                                                                                                                                   FQYIEGEMRTRIRYNRRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    576 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                 (updated)
(first entry)
               /label= Sig_peptide 36..302
/label= A-domain
                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 1020; DB 8; 100.0%; Pred. No. 1.4e-99;
                                                                                                                                                                                                                                                                                                                                                                                                   233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 576;
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                                                                                                                               Qy
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                                                                                                                                                                                        QΥ
                                                                                                                                                                                                                                                                                                          This polypeptide comprises the castorbean cytotoxin, ricin.

CDNA (see AAT91638) encoding the enzymatic A domain and a portion CC of the A-to-B linker peptide of ricin was used to construct a cricin-diphtheria toxin B'-interleukin-2 gene that was expressed in CC conditions involving over-production of cells bearing IL2 receptors, CC conditions involving over-production of cells bearing IL2 receptors, CC such as certain T-cell lymphomas and organ transplant rejection CC rises. The hybrid inactivates ribosomes in cells bearing IL2 creeptors, resulting in cessation of protein synthesis and death of CC target cells. Claimed hybrid proteins comprise a translocation CC domain and a cell binding domain from e.g. a hormone, growth factor CC or polypeptide toxin. The hybrid molecules can be used for the CC (labels) into cells. The use of a translocation mechanism ensures CC that the hybrid will be effective in relatively low doses, since a high proportion of the substance of interest will be taken into the CC targeted cells. The hybrid molecules can be manufactured as a CC single hybrid recombinant protein, permitting reproducibility, CC consistency, and the precise control of composition.
                                                                                                                                                                                                                          Query Match
Best Local S
Matches 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JUN-1985;
22-DEC-1989;
14-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  27-JUN-1991;
07-JUN-1984;
25-APR-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US5668255-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New hybrid molecules for delivery of agents to cells - comp
binding domain of a cell binding ligand and a portion of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAT91638.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1997-470103/43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SERA-) SERAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; Fig llA-B; 30pp; English.
                                                                                                                                                                                                                                                                                    Sequence
                                                                         121
                                                                                                                                                                                                                             198;
                181
                                                                                                        96
                                                                                                                                    61
                                                                                                                                                                   36
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                                                                                                                                                                                                                                         Similarity
                                                            GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
                                                                                                     IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIFVLPNRVGLPINQRFILV
FQYIEGEMRTRIRYNRRS
                                              GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
                                                                                                                                                                   IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                      576 AA;
                                                                                                                                                                                                                          100.0%; Score 1020; DB 18; llarity 100.0%; Pred. No. 1.4e-99; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85US-0742554.
89US-0456095.
90US-0538276.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84US-0618199
85US-0726808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91US-0722484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               303..314
/label= Linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= B-domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of a protein
                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                         Length 576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          comprise
                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                             Gaps
                                                                              180
                                                                                                        155
                                                                                                                                       120
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RESULT 13
AAY55892
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                                                                                                                              The invention relates to a recombinant DNA molecule encoding a hybrid coprotein comprising three parts: (a) the first part comprises a portion of the binding domain of a cell-binding polypeptide ligand allowing the chybrid protein to bind to an animal cell; (b) the second part comprises comparises a portion of a translocation domain of a naturally occurring protein context, IT toxin, C3 toxin, botulinum neurotoxin, ricin, cholera context, IT toxin, C3 toxin, biga-like toxin, pertussis toxin and tetanus context, which translocate the third part of the across the cytoplasmic commitment into the cytosol of the cell; and (c) the third part comprises compared to the naturally occurring protein of (b). This sequence represents the context of the cell of the cell, which is non-native convertion. The hybrid molecule enables the direction of appropriate convention. The hybrid molecule enables the direction of appropriate convention of the disease. The hybrid is especially used in treating cellular enzyme to affected cells, allowing them to function properly and convention diseases, by delivering to affected cells an enzyme conventional convention according to a scarce precursor or cofactor, to directing toxins convention according to affected cells of a scarce precursor or cofactor, to directing toxins convention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-APR-1985;
07-JUN-1985;
22-DEC-1989;
14-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translocation domain; botulinum; neurotoxin; rich; cholera; tetar shiga-like toxin; pertussis; translocation; cytoplasmic membrane; cytosol; therapy; genetic deficiency disease; enzyme; co-factor; padipocyte; cancer; virus; infection; antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY55892 standard; Protein; 576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-632431/54.
N-PSDB; AAZ30663.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murphy JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JUN-1984;
27-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ricinus communis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Castor bean ricin toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-FEB-2000 (first entry)
                                                        or other poisons to destroy particular cells (such as adipocytes, cancer cell, or virus infected-cells), to counteracting viral infections such as HIV, by introducing appropriate antibodies to viral proteins. It is also involved in the process of getting non-therapeutic substances such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 4; Fig 11; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant DNA molecule encoding a three part hybrid protein used the treatment of Alds and genetic deficiency diseases - \!\!\!\!\!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-OCT-1999
                                       detectable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SERA-) SERAGEN INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216 FQYIEGEMRTRIRYNRRS 233
                                         labels into cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hybrid; binding domain; ligand; animal cell; diphtheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93US-0102387.
84US-0618199.
91US-0722484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85US-0726808.
85US-0742554.
89US-0456095.
90US-0538276.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
This sequence represents the Ricinus communis ricin protein sequence. The toxin can be included in the hybrid protein of the invention and used to destroy or modify the cell that the hybrid protein is targeted to. The hybrid protein comprises a first part which is a portion of the binding domain of a cell-binding ligand, effective to cause the hybrid molecule to bind to a cell of an animal. The second part comprises a portion of a translocation domain of a naturally occurring protein (e.g. the translocation domain of diphtheria toxin) the second part translocates the third part across the cytoplasmic membrane and into the cytosol of
                                                                                                                                                                                                                                                       22-DEC-1989;
14-JUN-1990;
04-AUG-1993;
                                                                                                                                         New two-part hybrid protein comprising a translocation domain and cell-binding domain, for treating genetic deficiency diseases, car
                                                                                                                                                                                                                                                                                       25-APR-1985;
07-JUN-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                           Ricin; toxin; hybrid protein; translocation domain; cell destruction; cell binding domain; genetic deficiency disease; cell targetting; can adipocyte; enzyme delivery; anti-viral; HIV.
                                                                                                           Example 4; Fig 11; 32pp; English.
                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                             Murphy JR
                                                                                                                                                                                                                                 (SERA-)
                                                                                                                                                                                                                                                                                                             07-JUN-1984;
27-JUN-1991;
                                                                                                                                                                                                                                                                                                                                             07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                          Ricinus communis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ricinus communis ricin protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY78592;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY78592 standard;
                                                                                                                                                                                       2000-160390/14.
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91US-0722484.
85US-0726808.
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89US-0456095.
90US-0538276.
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                                                                                                                                                                                                                                                                                      Castor bean plant; preproricin; ricin; A chain; B chain; human immunodeficiency virus infection; HIV; toxin; antiviral agent; retroviral infection; anti-HIV; virucide activity; viral protease.
                                            WO200160393-A1
                                                                                                     Protein
                                                                                                                                             Peptide
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                                                                                                    /note=
                                                                                                                                               /note= "N-glycosidase" 303..314
                                                                                                               /label= Linker_peptide
/note= "Cleaved during
                                                                                                                                                                        /label= Ricin_A_chain
                                                                                                                                                                                                    /label= Signal peptide
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15-FEB-2001; 2001WO-US05282.

16-FEB-2000; 2000US-0182759

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Search completed: September 16, 2003, 11:45:17 Job time: 33.9711 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence relates to preproricin protein encoded by the DNA sequence compared in AAI64138. The invention relates to a novel toxin (e.g., ricin) compared antiviral agent which is toxic to virus-infected cells, but con-toxic to uninfected cells. The invention has anti-HIV and virucide activities. Its mechanism of action is through inactivation of cellular ribosomes and enhancement of binding of the antiviral agent to galactose considues on cell surfaces, and its cellular internalisation. The collular internalisation is useful for treating human immunodeficiency virus infection compared to an other viral infections, especially retroviral infections. The contiviral agent is activated in viral particles or early-stage infected colls, killing the cells upon infection and effectively preventing the latency/rebound problem. The agent enters all HIV susceptible cells, cand not just cells known to act as host cells for the virus. The coll after the virus agent remains inert in a cell until degraded in it, unless the coll is infected with the virus, where the viral protease activates it.
                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 198; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel composition comprising toxin e.g., ricin based antiviral compound useful for treating viral infections such as human immunodeficiency virus infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 50-54; 66pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-581908/65.
N-PSDB; AAI64138.
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                                                                                     216 FQYIEGEMRTRIRYNRRS 233
                                                                                                                             181 FQYIEGEMRTRIRYNRRS 198
                                                                                                                                                                                           121 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 180
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                                                                                                                                                                                                                                                      96 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 1020; DB 22; Length 576; 100.0%; Pred. No. 1.4e-99;
                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

September 16, 2003, 11:30:32; Search time 6.94128 Seconds (without alignments) 1341.437 Million cell updates/sec

Title: Perfect score:

US-10-083-336A-3 1020 1 IFPKQYPIINFTTAGATVQS.....ARFQYIEGEMRTRIRYNRRS 198

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_41:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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45	44	43	42	41	40	39	38	37	36	35	34
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7.5	7.7	7.7	7.9	8.1	8.3	8.4	8.8	8.8	9.7	10.1	10.5
157	493	485	305	492	609	1165	315	315	560	304	301
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RIP4_SAPOF	AERA_AERHY	AER5_AERHY	Y348_MYCPN	AERA_AERTR	FTSH_TREPA	SYV_AQUAE	SLTA_BPH30	SLTA_BPH19	JI60_HORVU	RIP9_MAIZE	RIPX_MAIZE
P27561 saponaria o		Q06306 aeromonas h	P75255 mycoplasma	P09166 aeromonas t	083746 treponema p	067411 aquifex aeo	P10149 bacteriopha	P08026 bacteriopha	Q00531 hordeum vul	P25892 zea mays (m	P28522 zea mays (m

## ALIGNMENTS

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[/] REVIEW. MEDLINE=21480122; PubMed=11595634; Olsnes S., Kozlov J.V.;	BOHYDRATE-LINKAGE LINE-90344223; Pul ura Y., Kusuoku H ructural analyses ic. Biol. Chem. 5	SEQUENCE OF 315-576.  SEQUENCE OF 315-576.  Funatsu G., Kimura M., Funatsu M.;  Primary structure of Ala chain of ricin D.";  "Primary structure of Ala chain of ricin D.";  Agric. Biol. Chem. 43:2221-2224(1979).	SEQUENCE OF 36-302.  SEQUENCE OF 36-302.  Yoshitake S., Funatsu M.;  Yoshitake S., Funatsu G., Funatsu M.;  "Isolation and sequences of peptic peptides, and the complete sequence of Ile chain of ricin-p.";  Sequence of Ile chain of ricin-p.";  Agric. Biol. Chem. 42:1267-1274(1978).	SEQUENCE OF 12-576 FROM N.A.  SEQUENCE OF 12-576 FROM N.A.  MEDLINE-85179479; PubMed=3838723;  MEDLINE-85179479; PubMed=3838723;  Lamb A., Roberts L.M., Lord J.M.;  "Nucleotide sequence of cloned cDNA coding for preproricin.";  Eur. J. Blochem. 148:265-270(1985).	SEQUENCE FROM N.A.  MEDILINE-92163016; PubMed=1371405; Tregear J.W., Roberts L.M.; Trehe lectin gene family of Ricinus communis: cloning of a functional ricin gene and three lectin pseudogenes."; Plant Mol. Biol. 18:515-525(1992).	SEQUENCE FROM N.A.  MEDLINE-86067214; PubMed=2999712;  Halling K.C., Halling A.C., Murray E.E., Ladin B.F., Houston L.L.,  Weaver R.F.;  "Genomic cloning and characterization of a ricin gene from Ricinus communis.";  Nucleic Acids Res. 13:8019-8033(1985).	79; P02880; 101-1986 (Rel. 01, Created) 101-1987 (Rel. 05, Last sequence updat EP-2003 (Rel. 42, Last annotation upd n precursor [Contains: Ricin A chain 3.2.22); Ricin B chain]. nus communis (Castor bean). ryota; Viridiplantae; Streptophyta; E ryota; Viridiplantae; Streptophyta; E marophyta; Magnollophyta; eudicotyled sids I; Malpighiales; Euphorbiaceae; TaxID-3988;	RICI RICCO STANDARD: PRT: 576 AA

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MEDLINE=96374222; PubMed=8780513;
Day P.J., Ernst S.R., Frankel A.E., Monzingo A.F., Pascal J.M.,
Molina-Svinth M.C., Robertus J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=91352004; PubMed=1881881;
Katzin B.J., Collins E.J., Robertus J.D.
"Structure of ricin A-chain at 2.5 A.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Monfort W., Villafranca J.E., Monzingo A.F., Ernst S.R., Katzin B., Rutenber E., Xuong N.H., Hamlin R., Robertus J.D.; "The three-dimensional structure of rich at 2.8 A.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rutenber E., Robertus J.D.;
"Structure of ricin B-chain at 2.5-A resolution.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-87165983; PubMed=3558397;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Toxicon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochemistry 35:11098-11103(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Analysis of several key active site residues of ricin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93165632; PubMed=1287657;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Structure-based identification of r. Mol. Biol. 266:1043-1049(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Robertus J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97240820; PubMed=9086280;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Structure and activity of an active site substitution of ricin A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       K-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF MUTANT HIS-215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "X-ray structure of recombinant ricin A-chain at 1.8-A resolution.", Mol. Biol. 244:410-422(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pauptit R.A.;
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for cell agglutination. The galactopyranoside moleties.

CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at catalytic active moleties.

Specific adenosine on the 28S rRNA.

SUBUNIT: Disulfide-linked dimer of A and B chains.

SUBUNIT: Disulfide-linked dimer of A and B chains.

DOMAIN: The B chain is composed of two domains, each domain consists of 3 homologous subdomains (alpha, beta, gamma).

PTM: THE MAJOR A-CHAIN IS GLYCOSYLATED ALSO IN POSITION 271.

MINOR A-CHAIN IS GLYCOSYLATED ALSO IN POSITION 271.

SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X., Hollis T.,
                                                                                                                                                                                                                                                                                                                                                                            synthesis. The A chain can inactivate a few thousand ribosomes per minute, thus inactivating them faster than the cell can make per words. A single A-chain molecule can therefore kill an animal cell. The B chain binds to cell receptors and facilitates the entry into the cell of the A chain; B chains are also responsible for cell agglutination (Lectin activity). It binds to beta-D-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Ricin is higly toxic to animal cells and to a less extent to plant cells. The A chain is responsible for inhibiting protein synthesis through the catalytic inactivation of 60S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  specific adenine residue from an exposed loop of 28S ribosomal RNA. As this loop is involved in the binding of elongation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ribosomal subunits. It acts as a glycosidase that removes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        factors, the modified ribosomes are unable to support protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39:1723-1728(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Robertus
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EMBL; X52908; CAA37095.1;
EMBL; X02388; CAA26230.1;
EMBL; A12892; CAA01058.1;
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DOMAIN
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CHAIN
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Pfam; PF00161; RIP; 1.
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SIGNAL
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InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: Contains 2 ricin B-type lectin domains.
CAUTION: REF.4 AND REF.5 SEQUENCES HAVE A HIGH NUMBER OF CONFLICTS
WITH THE SEQUENCE TRANSLATED FROM DNA (REF.1, REF.2 AND REF.3).
DATABASE: NAME-Protein Spotlight;
NOTE-Issue 31 of February 2003;
                                                                                                                                                                                                                                                                                                                                                                                                            ; A24041; RLCSD.

2AA1; 31-7AN-94.

1APG; 31-7AN-94.

1IFW; 31-0CT-93.

1IFS; 14-7AN-98.

1IFT; 14-7AN-98.

1IFU; 14-7AN-98.

1IFU; 14-7AN-98.

1IRU; 14-7AN-98.

1RTC; 31-0CT-93.

1OBS; 16-7UN-97.

1OBT; 16-7UN-97.

1OBT; 16-7UN-97.

1OBT; 16-7UN-97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restr by non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                         1BR5;
1BR6;
1IL3;
                                                                                                                                                                                                                                                                                                         SM00458; RICIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 non-profit institutions as long and this statement is not removed.
                                                                                                                                                                                                                                                                                     PS50231; RICIN_B_LECTIN; 2.
PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                     16-JAN-02;
16-JAN-02
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303
315
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377
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                                                                                                                                                                                                                                                                      Lectin;
                                                                                                                                                                                                                                                                              Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
                                                                                                                                                                                                                                                                                                                   SHIGARICIN.
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449
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570
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318
353
394
478
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                 N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
E -> D (IN REF. 3).
A -> R (IN REF. 3).
                                                     N-LINKED (GLCNAC. /FTId-CAR_00080. N-LINKED (GLCNAC. /FTId-CAR_00081.
                                                                                                                                                                                                            LINKER PEPTIDE.
RICIN B CHAIN.
RICIN B-TYPE LECTIN 1
RICIN B-TYPE LECTIN 2
                                                                                                                                                                                  1-BETA.
1-GAMMA.
                                                                                                                                                      2-GAMMA.
                                                                                                                                                               2-BETA
                                                                                                                                                                          2-ALPHA.
                                                                                                                                                                                                                                                    RICIN A CHAIN
                                                                                                                                     INTERCHAIN
                                                                                                                                                                                                                                                                      3D-structure.
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Toxin; Repeat;

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RESULT 2
AGGL_RICCO
ID AGGL_R
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DT 01-JAN
DT 02-JAN
DT 28-FEB
DE AGGUEN
CO SRICLINU
CO ENKARY
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Best Local
                                                                                                                                                                                    Lin T.T. S., Li S.-L.;
Lin T.T.-S., Li S.-L.;
Purification and physicochemical properties of ricins and agglutinins from Ricinus communis.";
Bur. J. Biochem. 105:453-459(1980).
-I- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at opening the specific adenosine on the 28S TRNA.
-I- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
-I- SIMILARITY: Contains 2 ricin B-type lectin domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ol-JAN-1988 (Rel. 06, Created)
Ol-JAN-1988 (Rel. 06, Last sequence update)
28 FEB-2003 (Rel. 41, Last annotation update)
28 FEB-2003 (Rel. 41, Last annotation update)
Agglutinin precursor (RCA) (Contains: Agglutinin A chain (rRNA)
glycosidase) (EC 3.2.2.2); Agglutinin B chain].
Ricinus communis (Castor bean).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophy
Eppermatophyta; Maggnollophyta; eudicotyledons; core eudicots; Ro
eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
           EMBL; M12089;
EMBL; S40368;
                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                    Araki T., Yoshioka Y., Funatsu G.;
"The complete amino acid sequence of the B-chain of the Ricinus communis agglutinin isolated from large-grain castor bean seeds."; Biochim. Biophys. Acta 872:277-285(1986).
                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=80178723; PubMed=6768555;
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 303-337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-86059449; PubMed-2999130;
Roberts L.M., Lamb F.I., Pappin D.J.C., Lord J.M.;
"The primary sequence of Ricinus communis agglutin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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       AAA33869.1; -.
AAB22584.1; -.
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Pred. No. 2.4e-87;
Mismatches 0;
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                                                                         (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  agglutinin.
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STANDARD; PRT; 562 AA.
P28590;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
Abrin-c precursor [Contains: Abrin-c A chain
(EC 3.2.22); Abrin-c B chain].
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InterPro; IPR001574; RIP.
Pfam; PF00552; Ricin_B_lectin; 6.
Pfam; PF00161; RIP; 1.
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SIGNAL
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91.9%;
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licorice) (Crab's eye)
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INTERCHAIN (BY SIMILARITY).
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N -> D (IN REF. 2).
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R -> T (IN REF. 2).
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InterPro; IPR001574; RIP.
Pfam; PF00552; Ricin_B_lectin; 6.
Pfam; PF00161; RIP; 1.
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PROSITE; PS00275; SHIGA_RICIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                              62817 MW;
      34.7%;
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ABRIN C B CHAIN (BY SIMILARITY)
RICIN B-TYPE LECTIN 1.
RICIN B-TYPE LECTIN 2.
      Score 353.5;
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INTERCHAIN (BY SIMILARITY).
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                                                               GLCNAC . . .)

GGLCNAC . . .)
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Abrin-b precursor [Contains: Abrin-b A chain |
(EC 3.2.2.22); Abrin-b B chain].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

MEDLINE=93132798; PubMed=8421313;

Hung C.-H., Lee M.-C., Lee T.C., Lin J.-Y.;

"Primary structure of three distinct isoabrins determined by cDNA sequencing. Conservation and significance.";

J. Mol. Biol. 229:263-267(1993).
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                                                                                                                                                     ABRB_ABRPR
            use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                            "The complete amino acid sequences of the B-chains of abrin-a and abrin-b, toxic proteins from the seeds of Abrus precatorius."; Biosci. Biotechnol. Biochem. 57:166-169(1993).

-!- FUNCTION: THE A CHAIN IS REPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA.
                                                                                   the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kimura M., Sumizawa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93169023; PubMed=7763422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 260-527.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Abrus precatorius (Indian licorice) (Crab's eye)
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                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond
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                                                                                                                                                                                                                                                                                              PRECEDES ENDOCYTOSIS.
                                                                                                                                                                                                                                                                                                              FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT
                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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4; Mismatches 70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001574; RIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000772;
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p; P11140;
                                                                                                                 125 RLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYI
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SM00458; RICIN; 2.
                                                                                                                                                                                                                                                                                                                                           87;
                                                                                                                                                                                                                                                                                                                                                            Similarity
SYRVGVSIRTN 181
                                                                                                                                                                                        HAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYD
                                                                                                                                                                                                                                                QDQVIKFTTEGATSQSYKQFIEALRQRLTGG--LIHGIPVLFDFTTLQERNRYISVELSN
                                          EGEMRTRIRYN 195
                                                                             DLERLARQTRQQIPLGLQALRHAISFL----QSGTDDQETARTLIVIIQMASEAARYRFI
                                                                                                                                                                  SDTESIEAGIDVSNAYVVAYRAGNRSYFL---
                                                                                                                                                                                                                                                                                          QYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSN
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45.5%;
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N-Y D (IN REF. 2)
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POTEN

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N-LINKED (GLCNAC. . .) (POTEN
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Pred. No. 1
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B-TYPE LECTIN 2.
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AC P09989;
AC P09989;
DT 01-MAR-1989
DT 01-NOV-1990
DT 15-SEP-2003
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OS TICLOSOMENTO
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RC STRAIN-MAXIN
RX MEDLINE-901:
RA Shaw P.C.,
RT Cloning of
RT Coli.";
RL Gene 97:267
RT SEQUENCE FR
RC STRAIN-MAXIN
RX MEDLINE-902:
RA STRAIN-MAXIN
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RA WANG Y. QLI
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RA WANG Y. QLI
RA TIAN G.Y.,
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Huang Q., Liu S., Tang Y., Jin S., Wang Y.;
"Studies on crystal structures, active-centre geometry and depurinating mechanism of two ribosome-inactivating proteins.";
Biochem. J. 309:285-298(1955).
-i- FUNCTION: TRICHOSANTHIN IS AN ABORTION-INDUCING PROTEIN. IT IS CAPABLE OF INHIBITING HIV-1 INFECTION AND REPLICATION. IT INACTIVATES EUKARVOTIC 60S RIBOSOMAL SUBUNITS.
-i- CATALYTIC ACTUVITY: Endohydrolysis of the N-glycosidic bond at Specific adenosine on the 28S IRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Scientific evaluation of Tian Hua Fen application.";
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01-NOV-1990 (Rel. 16, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ribosome-inactivating protein alpha-trichosanthin
(rRNA N-glycosidase) (EC 3.2.2.2) (Alpha-TCS).
Trichosanthes kirilowii (Mongolian snake-gourd).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proteins 19:4-13(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhou F., Fu Z., Chen M., Lin Y., Pan K.;
"Structure of trichosanthin at 1.88-A resolution.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (1.88 ANGSTROMS).
MEDLINE=94344957; PubMed=8066085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang Y., Qian R.Q., Gu
Tian G.Y., Ni C.Z.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Tuberous root;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wu P., Hwang K., Piatak M.;
"Primary amino acid sequence of alpha-trichosanthin and molecular models for abrin A-chain and alpha-trichosanthin.";
J. Biol. Chem. 265:8665-8669(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Maximowicz; TISSUE=Tuberou
MEDLINE=90256789; PubMed=2341399;
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"Isolation and DNA sequence of a gene encoding alpha-trichosanthin, type I ribosome-inactivating protein.";

J. Biol. Chem. 265:8670-8674(1990).
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MEDLINE=91153657; PubMed=1
Shaw P.C., Yung M.H., Zhu
"Cloning of trichosanthin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
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                                                                                                                                                                                                                                   SIMILARITY:
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                                                                                                                                                                                                     1 RIP SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Robertus J.D., Lopresti M.,
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                                                                                                                                                                                                                             BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2.W., Jin S.W., Zhang L.Q., Xia Z.X.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .K., Ng T.B., Y
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Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
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1MRK;
1TCS;
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1NLI;
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rPro; IPR001574; RIP.
; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; M34858; AAA34207.1; -.; J05434; AAA34206.1; -. JT0566; RLTZT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-FEB-95.
07-FEB-95.
10-JUL-95.
28-JAN-03.
21-JAN-03.
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                                                                                                                                                                                                                                                 271
183
57
82
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92
 3D-structure.
 MISSING IN MATURE PROTEIN.
BY SIMILARITY.
IPLL -> LPLI (IN REF. 4).
I-> L (IN REF. 4).
I-> L (IN REF. 4).
V -> UDGLEPRAVL (IN REF. 4).
KI -> GL (IN REF. 4).
K -> GL (IN REF. 4).
K -> T (IN REF. 4).
WS -> LML (IN REF. 4).
S -> T (IN REF. 4).
S -> T (IN REF. 4).
S -> T (IN REF. 4).
S -> MISSING (IN REF. 4).
INSING (IN REF. 4).
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RIP2_BRYDI
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SEQUENCE
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribosome-inactivating protein bryodin II precursor (rRNA
glycosidase) (EC 3.2.2.22) (BD2).
                                                                                                    This SWI
between
                                     the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                        MEDIINE-95151812; PubMed=7849072;
Siegall C.B., Gawlak S.L., Chace D., Wolff E.A., Mixan B.,
Marquardt H.;
Mcharacterization of ribosome-inactivating proteins isolated
Bryonia dioica and their utility as carcinoma-reactive
                                                                                                                                                                                                                                                                                                                                                                                                                              bryonia dioica (Red bryony)
Bryonia dioica (Red bryony)
Bukaryota; Viridiplantae; Streptophyta; Embryophy
Spermatophyta; Magnoliophyta; eudicotyledons; cor
spermatophyta; eudicotyledons; eudicotyledons; cor
spermatophyta; eudicotyledons; eudic
                                                                                                                                                    Siegall C.B., Gawlak S.L., Marquardt H.; "Bryodin 2 a ribosome-inactivating protein isolated from the plant
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                                                                                                                                                                                                                                                                                                        TISSUE-Root
                                                                                                                                                                                                                                                                                                                  SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                         Patent number US5597569, 28-JAN-1997
                                                                                                                                                                                                                                                                                                                                                      Bryonia dioica."
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                                                                                                                                          TYPE 1 RIP SUBFAMILY.
                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
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      P09989;
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Pred. No. 1.3e-24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ribosome-inactivating protein karasurin precursor (rRNA N-glycosidase) (EC 3.2.2.2).
Trichosanthes kirilowii (Mongolian snake-gourd).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
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                                                                                                                                                                                                                                                   60S RIBOSOMAL SUBUNITS.

-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rrna.

-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 24-270.
MEDLINE=92005921; PubMed=1914000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mizukami H., Iida K., Kondo T., Ogihara Y.;
"Cloning and bacterial expression of a gene encoding ribosome-inactivating proteins, karasurin-A and karasurin-C, from Trich kirilowii var. japonica.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-DEC-1998 (Rel. 37, Last sequence update) 28-FEB-2003 (Rel. 41, Last annotation updat
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PROSITE; PS00275; SHIGA_RICIN; 1.
Plant defense; Protein synthesis inhibitor; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                 Chem. Pharm. Bull. 39:1244-1249(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Toyokawa S., Takeda T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The complete amino acid sequence of an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSVTLALDVTNAYVYGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLE 127
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ull. 20:711–713(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23;
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Pred. No. 1.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ogihara Y.;
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P33184; P93542;
01-OCT-1993 (Rel. 27, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last sequence update)
29-FEB-2003 (Rel. 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROPEP
ACT_SITE
SEQUENCE
                                                                  Girbes T., Citores L., Ferreras J.M., Rojo M.A., Iglesias Munoz R., Arias F.J., Calonge M., Garcia J.R., Mendez E.; "Isolation and partial characterization of nigrin b, a no novel type 2 ribosome-inactivating protein from the bark
                             Plant Mol. Biol.
                                                 nigra L.
                                                                                                                                                                                              TISSUE-Bark
                                                                                                                                                                                                                                                            (nigrin b), a GalNAc-specific type-2 ribosome-inactivating protein
from the bark of elderberry (Sambucus nigra).";
Eur. J. Biochem. 237:505-513(1996).
                                                                                                                                                                                                                                                                                                                               Van Damme E.J., Barre A., Rouge P., Van Leuven F., Peumans W.J.; "Characterization and molecular cloning of Sambucus nigra agglutinin
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Asteridae;
                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96215449; PubMed=8647092;
                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Bark
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4202;
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    -!- FUNCTION: NON-TOXIC TYPE 2 RIP WHICH
                                                                                                                                                                   MEDLINE=94003077; PubMed=8400135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plant defense; Antiviral;
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PIR; JU0393; JU0393.
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                                                                                                                                                                                                                  EQUENCE OF 26-49
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No. 3.1e-24;
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STRONGLY INHIBITS MAMMALIAN
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Pfam; PF00161; RIP; 1.
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InterPro; IPR001574;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S37382;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
        124 DRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQY
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                                                                                                                                            Similarity
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                                  NGNTVTLAVDVTNLYVVAFSGNANSYFF----KDATEVQKSNLFVGTKQN-TLSFTGNY
                                                       AELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAI--THLFTDVQNRYTFAFGGNY
                                                                                  YPSVSFNLDGAKSATYRDFLSNLRKTVATGTYEVNGLPVLRRESEVQVKSRFVLVPLTNY
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RESULT 9
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"Crystal structure of abrin-a at 2.14 A.";
J. Mol. Biol. 250:354-367(1995).
-I- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTE.
SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSI
SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S;
BUSUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S;
ABRIN-A IS MORE TOXIC THAN RICIN.
-I- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT
FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THA
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01-JUL-1989 (Rel. 11, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Abrin-a precursor [Contains: Abrin-a A chain
(EC 3.2.2.22); Abrin-a B chain].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. PubMed=8421313; MEDLINE=93132798; PubMed=8421313; Hung C.-H., Lee M.-C., Lee T.C., Lin J.-Y.; "Primary structure of three distinct isoabrins sequencing. Conservation and significance."; J. Mol. Biol. 229:263-267(1993).
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Spermatophyta; Magnoliophyta; eudicotyledons; core e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The complete amino acid sequence of the A-chain protein from the seeds of Abrus precatorius."; Agric. Biol. Chem. 52:1095-1097(1988).
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - \,
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Chen Y.-L., Chow L.-P., Tsugita A
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                                                                                                                                                                                                                                                                                                       -i- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at
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                                                                                                                                                  SPECIFIC AGENOSINE ON THE 28S TRNA.
SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN
CONSISTS OF 3 HOWOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSO
                                                                          INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY. SIMILARITY: Contains 2 ricin B-type lectin domains.
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PDB; IABR; 07-FEB-95.

InterPro; IPR000772; Ricin_B_lectin.

InterPro; IPR001574; RIP.

Pfam; PF00652; Ricin_B_lectin; 6.

Pfam; PF00161; RIP; I.
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SMART; SM00458; RICIN; 2.
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RESULT 10
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PT 01-027
PT 16-027
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PT 28-FEB
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Ribosome-inactivating protein bryodin I precursor (rRNA N-glycosidase)
(EC 3.2.22) (BD1).
Bryonia diolca (Red bryony).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P33185; Q9S819;
01-OCT-1993 (Rel. 27,
16-OCT-2001 (Rel. 40,
28-FEB-2003 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIP1_BRYDI
   This SWISS-PROT entry is copyright.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-95151812; PubMed=7849072; Siegall C.B., Gawlak S.L., Chace D., Marquardt H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Molecular, biological, and preliminary structural analysis of recombinant bryodin 1, a ribosome-inactivating protein from the plant Bryonia dioica.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=89326691; PubMed=2753596;
Montecucchi P.C., Lazzarini A.M., Barbieri L., Stirpe F., Soria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gawlak S.L., Neubauer M., Klei H.E., Chang C.Y.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bryonia dioica and their utility as carcinoma-reactive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 24-43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent number US5541110,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Siegall C.B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Siegall C.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97228081; PubMed=9115985;
                                                                                                                                                                                                                                                                                                                                                                                          immunoconjugates.";
Bioconj. Chem. 5:423-429(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Characterization of ribosome-inactivating proteins isolated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "N-terminal sequence of some ribosome-inactivating proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cloning and expression of a gene encoding bryodin 1 from Bryonia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochemistry 36:3095-3103(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=3652;
                                                                                pharmacological applications as it has low toxicity in rats and mice but is potent once inside target cells.
SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY
                                                                                                                                                                                                         CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 285 frNA.

PTM: APPEARS TO UNDERCO PROTEOLYTIC CLEAVAGE IN THE C-TERMINAL TO PRODUCE A SHORTER PROTEIN.
                                                                                                                                                                                                                                                                                                                            conj. Chem. 5:423-429(1994).
FUNCTION: RIBOSOME-INACTIVATING PROTEIN SYNTHESIS IN ANIMAL CELLS
                                                                                                                                                                                BIOTECHNOLOGY: Especially useful as immunotoxin for
                                                              TYPE 1 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Pept.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cucurbitales; Cucurbitaceae; Bryonia
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                              PROTEIN OF TYPE 1, INHIBITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wolff E.A., Mixan B.,
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      is produced through a collaboration
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Query Match
Best Local S
Matches 69
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ACT_SITE
CARBOHYD
                                                                                                                                                                                                                                                                                                                                     MUTAGEN
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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HELIX
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InterPro; IPR001574; RIP.
Pfam; PF00161; RIP; 1.
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                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                   3D-structure; Multigene family; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00275; SHIGA_RICIN; 1.
Plant defense; Protein synthesis inhibitor; Hydrolase; Toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00396; SHIGARICIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; I24020; -; NOT_ANNOTATED_CDS.
                                                                       TURN
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                            SEQUENCE
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                             290
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66
66
66
67
70
82
82
82
83
11
10
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                                                                                           268
31788 MW;
       30.6%; Score 312; DB 1; 37.3%; Pred. No. 8.2e-22;
                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC...) (
N-LINKED (GLCNAC...) (
E->K: REDUCES ACTIVITY 1
RSSIS -> LRHXI (IN REF.
                                                                                                                                                                                                                                                                                                                                                                              RIBOSOME-INACTIVATING PROTEIN BRYODIN I. MISSING IN MATURE PROTEIN.
                             E966CD9C031A42DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY
              Length 290;
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10-FOLD.
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Conservative

46;

Mismatches

Indels

12;

Gaps

5

Similarity

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RESULT 11
RIPB_L
RIPB_R
RIPB_L
RIPB_R
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Best Local S
Matches 64
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ACT_SITE
SEQUENCE
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HSSP; P16094; 1AHC.
InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Islam M.R. Hirayama H., Funatsu G.;
"Complete amino acid sequence of luffin-b, a ribosome-inactivating protein from sponge gourd (Luffa cylindrica) seeds.";
Agric. Biol. Chem. 55:229-238(1991).
- CATALYTIC ACTIVITY: Encohydrolysis of the N-glycosidic bond at one specific adenosine on the 28s rRNA.
-1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 19, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribosome-inactivating protein luffin-B (rRNA N-glycosidase)
(EC 3.2.2.22).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Luffa cylindrica (Smooth loofah) (Sponge gourd).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids I; Cucurbitales; Cucurbitaceae; Luffa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00161; RIP; 1.
PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1991 (Rel.
01-AUG-1991 (Rel.
28-FEB-2003 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=91248488; PubMed=1368666;
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                                                   189
                                                                                                                                                                      129
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                                                                                                                                              LAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEM 188
                                                                                                                                                                                                                            AITMAIDVTNVYIMGYLVNSTSYF---ANESDAKLASQYVFKGSTLVTIPYSGNYERLQN 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MRTRI 192
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                                                   RTRIRYN 195
                                                                                                                                                                                                                                                                                   SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQ 128
                                                                                                                                                                                                                                                                                                                                            VSFSLSGADSKSYSKFITALRKALPSKEKVSNIPLLLPSASGA---SRYILMQLSNYDAK 59
                                                                                                                                                                                                                                                                                                                                                                                                   INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSFRLSGATTTSYGVFIKNLREALPYERKV-YNIPLL--RSSISGSGRYTLLHLTNYADE
IERIPKN 178
                                                                                                            AAGKIREKIPLGFRALDSALTSIFHYDS----TAAAAAFLVILQTTAEASRFKYIEGQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            250 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160
27293 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 300.5; D
Pred. No. 8.1e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
F01A8DC8A1078700 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             250 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8
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RESULT 12
RIP1_CUCFI
ID RIP1_CUCFI
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Best Local
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CARBOHYD
                                                                                                                                                                                                                                                                                             CHAIN
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9FRX4:

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)

Putative ribosome-inactivating protein precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core energiate; Cucurbitales; Cucurbitaceae; Cucumis. NCBI_TaxID-131071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cucumis figarei.
                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (EC 3.2.2.22).
                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                Plant defense; Antiviral;
                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00275; SHIGA_RICIN;
                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00396; SHIGARICIN.
                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00161; RIP;
                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB045560; BAB19677.1; -. HSSP; P16094; IAHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                     roxin;
                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE 1 RIP SUBFAMILY.
196
                                               141
                                                                                                                                                                                                                                                                                                                                                                                          P16094; 1AHC.
Pro; IPR001574; RIP.
                       188
                                                                                               84
                                                                                                                                                                        9
                                                                                                                                                                                                65;
                                                                                                                                                                                                                                                                                                                                    Signal
                                                                                                                                                                                                          Similarity
                       MRTRIRYNR 196
                                                                                                NTITMAVDVTNVYIMGYLVNGTSYFF---NETDAQLASKFVFQGTKSITLPYSGNYQKLQ
                                                                                                                     LSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLE
                                                                                                                                               VKFSLLGSNHKSYSKFITSMRNALPNAGDI-YNIPLLVPSISG---SRRYILMQLSNYEG
                                                                                                                                                            IIDRISVSK 204
                                                                       QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE
                                               SVARKERDSIPLGFMALDSAISTLYYYDSRSAPI----
                                                                                                                                                                                                                                                 286
                                                                                                                                                                                                                                                          1
22
185
103
110
252
                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                Ŗ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                          21
286
185
103
110
252
                                                                                                                                                                                                            29.1%;
                                                                                                                                                                                                                                                31771
                                                                                                                                                                                                                                                 ₩;
                                                                                                                                                                                                                                                                                                                                                 Protein synthesis inhibitor; Hydrolase;
                                                                                                                                                                                                47;
                                                                                                                                                                                                                                                        PUTATIVE RIBOSOME-INACTIVATING PROTEIN. BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                            Score 296.5;
Pred. No. 2.:
                                                                                                                                                                                                                                                                                                                       POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                4EFD4966E604DA41 CRC64;
                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
                                                                                                                                                                                                             .2e-20;
                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                64;
                                                 -AFLVLIQTTAEAARYKYIEKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (rRNA N-glycosidase)
                                                                                                                                                                                                Indels
                                                                                                                                                                                                                     Length 286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tracheophyta;
                                                                                                                                                                                                13;
                                                                        187
                                                                                                                                                                         67
                                                 195
                                                                                                                        127
                                                                                                                                                  83
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RESULT

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                          В
                                                Qy
                                                                                                                                MLA_VISAL
                                                                              Matches
                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Beta-galactoside specific lectin I A chain (MLA) (ML-I A) (rRNA N-glycosidase) (EC 3.2.2.2).
Viscum album (European mistletoe).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Santalales; Santalaceae; Viscum.
                                                                                                                                                                                                                                                              VARIANT
VARIANT
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEBS
                                                                                                                                                                                    VARIANT
VARIANT
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VARIANT
                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Subsp. album;
MEDLINE=97134581; PubMed=8980141;
                                                                                                                                                           VARIANT
                                                                                                                                                                       VARIANT
                                                                                                                                                                                                           VARIANT
                                                                                                                                                                                                                                                                                                        VARIANT
                                                                                                                                                                                                                                                                                                                     VARIANT
                                                                                                                                                                                                                                                                                                                                VARIANT
                                                                                                                                                                                                                                                                                                                                              CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                     Plant defense;
                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Complete amino acid sequence of the A chain of mistletoe lectin I.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Voelter W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Soler M.H., Stoeva S., Schwamborn C., Wilhelm S., Stiefel T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MLA_VISAL
                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CELL AGGLUTINATION (LECTIN ACTIVITY). CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 285\ \mathrm{rRNA}. SUBUNIT: Disulfide-linked dimer of A and B chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALTIC INACTIVATION OF 60S RIBOSOMAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RRNA. THE B CHAIN BINDS TO CELL RECEPTORS AND PROBABLY FACILITATES THE ENTRY INTO THE CELL OF THE A CHAIN; B CHAINS ARE ALSO RESPONSIBLE FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY TYPE 2 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHARMACEUTICAL: Due to its immunomodulative effects it is being studied in clinical trials in cancer patients as it may slow th growth of cancer cells and be an effective treatment for solid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AND NON-GLYCOSYLATED FORM MLA'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MISCELLANEOUS: TWO ISOFORMS OF MLA EXIST: GLYCOSYLATED FORM MLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                PD0018; PD0018.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lett. 399:153-157(1996)
                                                                                                                                                                                                                                                                                                                                                                                                           PF00161; RIP;
71 TLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLA 130
                                                    13
                                                                                                                                                                                                                                                                                                                                                                                                                                     P11140;
                          9
                                                                                                                                                                                                                                                                                                                                                                                             PR00396; SHIGARICIN
                                                                                        Similarity
                        THQTTGEEYFRFITLLRDYVSSGS-FSNEIPLL-RQSTIPVSDAQRFVLVELTNQGQDSV
                                                 TAGATVOSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPIN--QRFILVELSNHAELSV
                                                                                                                                                                                                                                                                                                                                                                                   PS00275;
                                                                                                                                                                                                                                                                                                                                                                                                                    IPR001574; RIP.
                                                                                                                                254 AA;
                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     1ABR
                                                                                                                                                                                                                                                                                                                                                                    Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                 SHIGA_RICIN;
                                                                                                                                                                                       T (IN MLA).

T (IN MLA).

T (IN MLA).

P -> T (IN MLA).

DQ -> EE (IN MLA).

T -> S (IN MLA).

T -> S (IN MLA).

Y -> D (IN MLA).

V -> E

V -> E
                                                                                        28.0%;
                                                                                                                                28478 MW;
                                                                           36;
                                                                                        Pred.
                                                                                         Score 286;
                                                                                                                                            U
                                                                                                                                                          T PP
                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. . .).
E -> D (IN MLA').
                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                 FALSE_NEG.
                                                                          Mismatches
                                                                                                                             53BAF98D3E0FFE67 CRC64;
                                                                                                                                                                      v
                                                                                                                                                                                                                                                                                                                                                                    Repeat;
                                                                                                                                                                                 F (IN MLA'
                                                                                                                                                                      ST
                                                                                                                                            (IN MLA'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       254
                                                                                                                                                                   (IN MLA').
                                                                                      DB 1;
.8e-19;
                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
                                                                           56;
                                                                                                   Length 254;
                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                     Lectin
                                                                           38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            slow the solid
                                                                        Gaps
                        66
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В
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RIPA_LUFCY
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                                                               Matches
                                                                                              Query Match
                                                                                                                              ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Last annotation update)
Ribosome Inactivating protein luffin-alpha prec
N-91/costdase) (EC 3.2.22).
Luffa cylindrica (Smooth loofah) (Sponge gourd)
Eukaryota; Viridiplantae; Streptophyta; Embryota
Spermatophyta; Magnoliophyta; eddicotyledons; co
eurosids I; Cucurbitales; Cucurbitaceae; Luffa.
                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                        entitles requires a license agreement (some send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kataoka J., Habuka N., Miyano M., Masuta C., Koiwai A.; "Nucleotide sequence of CDNA encoding alpha-luffin, a ribosome-inactivating protein from Luffa cylindrica."; plant Mol. Biol. 18:1199-1202(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-1992 (Rel. 24,
01-DEC-1992 (Rel. 24,
28-FEB-2003 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q00465;
                                                                                                                                                                                                                                                                        InterPro; IPRO01574; RIP. Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                           PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RIPA_LUFCY
                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                             Poxin; Signal.
                                                                                                                                                                                                                          Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
                                                                                                                                                                                                                                                                                                             HSSP; P16094; 1AHC.
                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92288316; PubMed=1600156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA. SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE 1 RIP SUBFAMILY.
                                                                                                                                                                                                                                                                                                                         S22494; S22494.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67
 22
                                 9
                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARF------Q 182
VRFSLSGSSSTSYSKFIGDLRKALPSNGTVYNITLLLSSASGA---SRYTLMTLSNYDGK
                               INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YINSGASFLPDVYMLELETSWGQQSTQVQHS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YIE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GH-RDQIPLGIDQLIQSVTALRF----PGGSTRTQARSILILIQMISEAARFNPILWRYRQ 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAAIDVTNAYVVAYQAGDQSYFLR-DAPRGAE--THLFTGT-TRSSLPFNGSYPDLERYA 122
                                                                                                                              179
277 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                               30212 MW;
                                                                                33.5%;
                                                                                              27.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
                                                                 45;
                                                                                              Score 284.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --GEMRTRIRYN 195
                                                                                                                                               BY SIMILARITY
                                                                                                                                                                             RIBOSOME - INACTIVATING
                                                                               Pred. No. 2.8e-19
                                                                                                                                                               ALPHA.
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                                                                                                                               EA17FC27998C25AC CRC64;
                                                               Mismatches
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                                                                                              277;
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69 79

AITVAVDVTNVYIMGYLVNSTSYFF---

SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQ 128

NESDAKLASQYVFKGSTIVTLPYSGNYEKLQT

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01-DEC-1992 (Rel. 24, C
01-DEC-1992 (Rel. 24, I
15-SEP-2003 (Rel. 42, I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ortigao M., Better M.;

"Momordin II, a ribosome inactivating protein from Momordica balsamina, is homologous to other plant proteins.";

Nucleic Acids Res. 20:4662(1992).

-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-1992 (Rel. 24, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ribosome-inactivating protein momordin II precursor (rRNA
N-glycosidase) (EC 3.2.2.22),
Momordica balsamina (Bitter gourd) (Balsam pear),
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid,
eurosids I; Cucurbitales; Cucurbitaceae; Momordica.
                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                             PDB; 1CF5; 07-JUN-99.
InterPro; IPR001574; RIP.
Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                     ACT_SITE
                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
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                                                                                                                                                                                                                                                                                                                3D-structure.
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                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; S25560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=3672;
                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE 1 RIP SUBFAMILY.
129 LAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEM 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOMBA
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                                82 TISVAIDVTNYYVVAYRTRDVSYFF---KESPPEAYNILFKGTR-KITLPYTGNYENLQT 137
                                                                                              25 VNFDLSTATAKTYTKFIEDFRATLPFSHKV-YDIPLLYSTIS--DSRRFILLDLTSYAYE 81
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                                                                                                                                                                                   Similarity
                                                                SYTLALDYTNAYYYGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQ 128
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32031 MW;
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286
                                                                                                                                                             27.4%; Score 279; DB 1; Length 286; 35.3%; Pred. No. 9.5e-19; tive 42; Mismatches 67; Indels
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193 AKYVATN 199
              RTRIRYN 195
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Search completed: September 16, Job time: 7.94128 secs 2003, 11:46:03

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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           401.5
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_invertebi:
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel1:
9: sp_plage:*
10: sp_plant:*
11: sp_rodent:
12: sp_virus:*
13: sp_vertebi:
14: sp_urclass:
15: sp_rvirus:*
16: sp_bacteri.
17: sp_archeap
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1 IFPKQYPIINFTTAG
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Match
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Gapop 10.0 , Gapext 0.5
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           IFPKQYPIINFTTAGATVQS.....ARFQYIEGEMRTRIRYNRRS 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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sp_phage:*
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sp_archeap:*
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sp_rvirus:*
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sp_rodent:*
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      Q41174
Q94BW4
Q94BW5
Q94BW5
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Q9FV22
Q9FV27
Q9AVR2
Q94VR2
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041174 ricinus com
094bw3 cinnamomum
094bw3 cinnamomum
094bw5 cinnamomum
094bw5 cinnamomum
094702 cinnamomum
004367 sambucus eb
006076 abrus preca
094ke4 trichosanth
091re3 trichosanth
038761 abrus preca
09452 sambucus ni
038761 abrus preca
081pv7 trichosanth
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45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
S.	9	62.		268	270	272	272	273	275	277	277	277.5	278	280	282	283	283.5	285	285	291	307.5	310.5	314.5	316.5	317	319	22	323.5
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573	293	299	603	300	592	298	286	249	531	569	286	565	293	264	254	251	604	570	249	570	278	566	547	251	270	565	251	251
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Q8W2E8	Q8VYU0	Q8GZN9	Q9M653	004356	Q8W2E7	004358	Q41257	Q8RXH7	Q8RXH6	P93543	Q9FUV7	Q8W243	Q8S452	Q9FSH2	Q8LKQ6	Q8LKQ4	Q9M654	022415	Q8LKQ5	Q41358	086000	004072	Q9M6E9	Q96235	Q41611	004071	Q96237	Q96236
Q8w2e8	Q8vyu0	Q8gzn9	Q9m653	004356	Q8w2e7	004358	Q41257	Q8rxh7	Q8rxh6	P93543	Q9fuv7	Q8w243	Q8s452	Q9fsh2	Q81kq6	Q81kg4	Q9m654	022415	Q81kq5	Q41358	086000	004072	Q9m6e9	Q96235	241611	004071	Q96237	Q96236
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## ALIGNMENTS

FT SQ	K C	7 P	DR	DR	DR	DR	DR	DR	DR	DR	DR	DR	င္ပ	င္ပင	cc	RL	RT	RA	RX	RP	RN	o <b>x</b>	8	റ്റ	ጸ	SO	DE	DE	DT	DT	DT	AC	ID	Q41174	RESULT
NON TER 1 SEQUENCE 541 AA; 60281 MW; 2B7B2CDEF1F2E9D9 CRC64;		PS00275;	PS50231;	SMART; SM00458; RICIN; 2.	PRINTS; PR00396; SHIGARICIN.	Pfam; PF00161; RIP; 1.				<pre>InterPro; IPR000772; Ricin_B_lectin.</pre>	HSSP; P02879; 1BR6.	EMBL; S40366; AAB22582.1;	-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.	SPECIFIC ADENOSINE ON THE 28S RRNA.	-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE	Targeted Diagn. Ther. 7:81-97(1992).	"Molecular cloning of ricin.";	Roberts L.M., Tregear J.W., Lord J.M.;	MEDLINE=92338377; PubMed=1633311;	SEQUENCE FROM N.A.	[1]	NCBI_TaxID=3988;	eurosids I; Malpighiales; Euphorbiaceae; Ricinus.	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	Ricinus communis (Castor bean).	(Fragment).	2.	23,	(TrEMBLrel. 01,	01-NOV-1996 (TrEMBLrel. 01, Created)	Q41174;	Q41174 PRELIMINARY; PRT; 541 AA.	.74	IJT 1

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RESULT 2

Q94BW
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Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Type 2 ribosome-inactivating protein cinnamomin III
(EC 3.2.22) (rRNA N-glycosidase).
Cinnamomum camphora (Camphor tree).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; Laurales; Lauraceae; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yang Q., Gong Z.Z., Liu W.Y.;
"Molecular cloning of three type 2 RIP (ribosome-inactivating progenes encoding cinnamomin proteins and study of their expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q94BW3
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SMART; SM00458; RICIN; 2.
PROSITE; PS50231; RICIN_B_LECTIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SIMILARITY: BELONGS TO THE RIBOSOME INACTIVATING PROTEIN FAMILY EMBL; AY039803; AAK82460.1; ...
InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=13429;
                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase;
SIGNAL
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Pfam; PF00161; RIP; 1.
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                                                                                                                  65 HAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYD 124
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                                                                                                                                                                                      6 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSN- 64
                                                                                                                                                                                                                                             94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FQYIEGEMRTRIRYNRRS 198
DLERVAGERREEILLGMDPLENAISALWISNL--NQQRALARSLIVVIQMVAEAVRFRFI
                                      RLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYI 184
                                                                              ADSPYTIAVDYTNAYVVAYRTGSQSFFLREDNPD--PAIENLLPDTK-RYTEPFSGSYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHDIPVLPNRVGLPINQRFILV
                                                                                                                                                            FQYIEGEMRTRIRYNRRS
                                                                                                                                                                                                                                                                                                                                                                                      Signal; Toxin.
                                                                                                                                                                                                                                                                                                                           580 AA;
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                                                                                                                                                                                                                                                                                                                           64421 MW;
                                                                                                                                                                                                                                                                  39.48;
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99.5%;
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Pred. No. 1
                                                                                                                                                                                                                                                                  Score 401.5;
Pred. No. 2.1
                                                                                                                                                                                                                                                                                                                                              TYPE 2 RIBOSOMI
CINNAMOMIN III
                                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                             940D10F01E7FB558 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                   2 RIBOSOME-INACTIVATING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   580 AA
                                                                                                                                                                                                                                                                  2.8e-29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .9e-87;
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                                                                                                                                                                                                                                                                                     DB 10;
                                                                                                                                                                                                                                           59;
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                                                                                                                                                                                                                                                                                   Length 580;
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Q94BW4
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Q94BW5
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O1-DEC-2001 (TrEMBLrel. 19, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Type 2 ribosome-inactivating protein cinnamomin II precursor
(EC 3.2.2.22) (rRNA N-glycosidase).
  Q94BW5;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Type 2 ribosome-inactivating protein cinnamomin I precursor
(EC 3.2.2.22) (rRNA N-glycosidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING EMBL; AY039802; AAK82459.1; -. InterPro; IPR000772; Ricin_B_lectin. InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yang Q., Gong Z.Z., Liu W.Y.;
"Molecular cloning of three type 2 RIP genes encoding cinnamomin proteins and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cinnamomum camphora (Camphor tree).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheoph
Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Cinnamomum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00396; SHIGARICIN.
SMART; SM00458; RICIN; 2.
PROSITE; PS50231; RICIN_B_LECTIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00652; Ricin_B_lectin;
Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Yang Q., Gong Z.Z.,
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                                                                                                                            Q94BW5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  patterns
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93;
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                                                                                                                                                                                                                                                                                                                                      RLEQLAGNIRENIEIGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYI 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EYRVRESI 214
                                                                                                                                                                                                                                                                                                            DLERVAGELREEILLGMDPLENAISAL--WTSNLNQQRALARSLIVVIQMVAEAVRERFI
                                                                                                                                                                                                                                                                                                                                                                                           AADSPVALAVDVTNAYVVAYRTGSQSFFLREDNPD--PAIENLLPDTK-RYTEPFSGSYT 148
                                                                                                                                                                                                                                  EYRVRESI 214
                                                                                                                                                                                                                                                                  EGEMRTRI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YQTVTFTTKNATKTSYTQFIEALRAQLASGEE-PHGIPVMRDGSTVPDSKRFILVELSNW
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Pred. No. 6.7
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TYPE 2 RIBOSOME-INACTIVATING
CINNAMOMIN II.
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DB 10;

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Best Local S
Matches 94
          Xie L., Liu W.-Y., Wang E.-D.;

"Molecular cloning of cinnamomin A., B-chain and the expression, purification, characterization and mutagenesis of the A-Chain.";

Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

-! CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT CATALYTIC ABENOSINE ON THE 28S RRNA.

-! STMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.

EMBL: AF25948; AF68978.2; -.
                                                                                                                                                                                                         N-glycosidase) (Fragment).
Cinnamomum camphora (Camphor tree).
Eukaryota, Viridiplantae; Streptophyta;
Spermatophyta; Magnoliophyta; Laurales;
NCBI_TaxID=13429;
                                                                                                                                                                                                                                                                                                   01-MAR 2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-CCT-2002 (TrEMBLrel. 22, Last annotation update)
Type II ribosome inactivating protein cinnamomin (E)
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Pfam; PF00161; RIP; 1.
PRINTS; PR00396; SHIGARICIN.
SMART; SM00458; RICIN; 2.
PROSITE; PS50231; RICIN_B_LECTIN; 2.
                                                                                                                                                  SEQUENCE FROM N.A.
Xie L., Liu W.-Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT (
SPECIFIC ADENOSINE ON THE 28S RNA.
-i- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY EMBL: AY039801; AAK82458.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. Liu W.Y.; Yang Q., Gong Z.Z., Liu W.Y.; Molecular cloning of three type 2
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Spermatophyta; Ma
NCBI_TaxID=13429;
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SIGNAL
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InterPro; IPR001574; RIP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EYRVRGSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGEMRTRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DLEGVAGERREEILLGMDPLENAISALWISNL--NQQRALARSLIVVIQMVAEAVRFRFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AADSPVTLAVDVTNAYVVAYRTGSQSFFLREDNPD--PAIENLLPDTK-RYTFPFSGSYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAELSYTLALDYTNAYYYGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YQTVTFTTKNATKTSYTQFIEALRAQLASGEE-PHGIPVMRERSTVPDSKRFILVELSNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          camphora (Camphor tree).
Viridiplantae; Streptophyta;
yta; Magnoliophyta; Laurales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      581
                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64215 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.0%; Score 397.5; DB 1 50.0%; Pred. No. 6.7e-29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
TYPE 2 RIBO
CINNAMOMIN
                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6E8F5FB8FBA3D196 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RIBOSOME - INACTIVATING
                                                                                                                                                                                                                                                                                                                                                                                                           549
                                                                                                                                                                                                                                                                                                         cinnamomin (EC 3.2.2.22) (rRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OF THE N-GLYCOSIDIC BOND AT ONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ribosome-inactivating protein)
study of their expression
                                                                                                                                                                                                                                Lauraceae;
                                                                                                                                                                                                                                                Embryophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lauraceae; Cinnamomum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                           B
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                                                                                                                                                                                                                                Cinnamomum
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                                                                                                                                                                                                                                              Tracheophyta;
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004367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-glycosidase).
Sambucus nigra (European elder).
Sumbucus nigra (European elder).
Eukaryota; Viridiplantae; Streptophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Ribosome inactivating protein precursor (EC 3.2.2.22) (rRNA
                                                  CHAIN
                                                                       Hydrolase;
SIGNAL
                                                                                                                                                PRINTS; PR00396; SHIGARICIN. SMART; SM00458; RICIN; 2.
                                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY EMBL; U76524; AAC15886.1; -. HSSP; P02879; 2AAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    004367;
01-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00396; SHIGARICIN. SMART; SM00458; RICIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00652; Ricin_B_lectin; Pfam; PF00161; RIP; 1.
              SEQUENCE
                                                                                                         PROSITE; PS50231; RICIN_B_LECTIN; PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                       Pfam; PF00652; Ricin_B_lectin;
Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                            InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                derived from a truncated to Plant J. 12:1251-1260(1997)
                                                                                                                                                                                                                                                                                                                                                                                  "The major elderberry (Sambucus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98112023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Spermatophyta; Magnoliophyta; eudicotyledons;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           004367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                -
                                                                                                                                                                                                                                                                                                                                                                                                                                            Van Damme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Asteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
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                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: ENDOHYDROLYSIS SPECIFIC ADENOSINE ON THE 28S RRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS50231; RICIN_B_LECTIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EYRVRGSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGEMRTRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AADSPVTLAVDVTNAYVVAYRTGSQSFFLREDNPD--PAIENLLPDTK-RYTFPFSGSYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAELSYTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YQTVTFTTKKATKTSYTQFIEALRAQLASGEE-PHGIPVMRERSTVPDSKRFILVELSNW
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                                ; Signal; Toxin.

1 25

26 297

298 563
                                                                                                                                                                                                                                                                                                                                                                                                                                         E.J.,
              563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           campanulids; Dipsacales; Adoxaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
              AΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Roy
                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=9450339;
oy S., Barre A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             192
              62336 MW;
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Pred. No. 9.5e-29;
                              POTENTIAL.
RIBOSOME INACTIVATING
RIBOSOME INACTIVATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                         6.
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              3ED2B6C08E796205
                                                                                                                                                                                                                                                                                                                                                                              nigra) fruit protein is a lectin
ribosome-inactivating protein.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Rouge
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Embryophyta;
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THE N-GLYCOSIDIC BOND AT ONE

CRC64;

PROTEIN, PROTEIN,

w >

CHAIN

Van Leuven

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core eudicots Sambucus

Tracheophyta;

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RESULT 7
QAVVZ
ID QAVVZ
AC QAVVZ
DT 01-J
DT 01
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                          Вb
                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9AVR2;
01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
R1bosome-inactivating protein precursor (EC 3.2.2.22) (rRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Girbes T., Iglesias R., Perez Y., Ferreras J.M., Citores L.;
"Molecular cloning of ebulin 1.";
"Molecular cloning of ebulin 1.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
-i- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spermatophyta; Magnollophyta; eudicotyledons; core eudic Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus (CBI_TaxID=28503;
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00652; Ricin_B_lectin; 6. Pfam; PF00161; RIP; 1. PRINTS; PR00396; SHIGARICIN. SMART; SM00458; RICIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Leaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sambucus ebulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-glycosidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9AVR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Glycosidase; Hydrolase; Signal; Toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50231; RICIN_B_LECTIN; 2. PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P02879; 2AAI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY L; AJ400822; CAC33178.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        142
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88
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                                                                                                                                                                                                                                                        78;
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                                                                                                                                                                                                                                                                                     Similarity
                                                           AELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAI--THLFTDVQNRYTFAFGGNY 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YPSYSFNLAGAKSATYRDFLKNLRTIVATGTYEVNGLPVLRRESEVQVKNRFVLVLLTNY 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IEGEMRTRIR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNLETAAGTRRESIELGPSPLDGAITSLYYDE----SVARSLLVVIQMVSEAARFRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGNTVTLAVDVTNLYVVAFSANANSYFF-----KDATQLQKSNLFVGTR-QHTLPFTGNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAI - THLFTDVQNRYTFAFGGNY 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH
                          NGDTVTSAVDVTNLYLVAFSANGNSYFF-----KDATELQKSNLFLGT-TQHTLSFTGNY 141
                                                                                                                                          YPSVSFNLAGAKSTTYRDFLKNLRDRVATGTYEVNGLPVLRRESEVQVKNRFVLVRLTNY
                                                                                                                                                                                             YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IEQEVRRSIQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                        564 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                298
                                                                                                                                                                                                                                                                                                                                                                        62694 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.4%;
                                                                                                                                                                                                                                                                                     34.1%;
41.1%;
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                                                                                                                                                                                                                                                                                  Pred.
                                                                                                                                                                                                                                                                                     Score 347.5; DB 10; Pred. No. 3.4e-24;
                                                                                                                                                                                                                                                                                                                                                                                                   EBULIN L A-CHAIN.
EBULIN L B-CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                        8261681A6DB55CB8 CRC64;
                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   564 AA
                                                                                                                                                                                                                                                                                  3.4e-24;
                                                                                                                                                                                                                                                        56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   core eudicots
                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                             Length 564;
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                                                                                                                                                                                                                                                        Gaps.
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Q06076
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                                                                                  Q94KE4
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                                                                                                             RESULT 9
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Best Local :
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Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-NOV-1996 (TrEMBLrel. 23, Last annotation update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Abrin-d (EC 3.2.2.2) (rRNA N-glycosidase) (Fragment).
Abrus precatorius (Indian licorice) (Crab's eye).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Fabales; Fabaceae; Papillonoideae; Abreae; Abrus.
Q94KE4;
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Mol. Biol. 229:263-267(1993).

1- CATALYTIC ACTIVITY: EMDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.

-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q06076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50231; RICIN_B_LECTIN; PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00652; Ricin_B_lectin; Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequencing: conservation and significance."; J. Mol. Biol. 229:263-267(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hung C.-H., Lee M.-C., Lee T.-C., Lin J.-Y.; "Primary structure of three distinct isoabrins determined by cDNA
                                                           Q94KE4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00458; RICIN; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00396; SHIGARICIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=93132798; PubMed=8421313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              185
                                                                                                                                                                                                                                                                                                                115 DLERWAHQTREEISLGLQALTHAIS---FLRSGASNDEEKARTLIVIIQMASEAARYRCI
                                                                                                                                                                                                                                                                                                                                                                     125 RLEQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYI 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   M98346; AAA32626.1;
P11140; 1ABR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 HAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYD 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5 QYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85;
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                                                                                                                                                                                                      SNRVGVSIR 180
                                                                                                                                                                                                                                                           EGEMRTRIR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                   SERESIEVGIDVTNAYVVAYRAGSQSYFL---RDAPASASTYLFPGTQ-RYSLRFDGSYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QDQVIKFTTEGATSQSYKQFIEALRQRLTGG---LIHDIPVLPDPTTVEERNRYITVELSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           528
528 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Toxin.
(TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                           PRELIMINARY;
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58870 MW;
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  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 344.5; DB Pred. No. 5.9e-24
                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62ED42FB8FFE60F8 CRC64;
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                                                              A
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528; 9

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Matches
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                                                                                                                                                                                                                                                                                           01-OCT-2000
01-OCT-2000
01-OCT-2002
                                      "Genomic DNA Clone for mature typ-1 ribosome-inactivating protein Trichosanthes sp. sample 01 Bac Kan 8-98 Vien CNSH (Hanoi)."; Submitted (FEB-2000) to the EMBLYGENBARY/DRBD databases.
-- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT SPECIFIC ADENOSINE ON THE 28S RRNA.
-- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
                              EMBL;
                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
                                                                                                                                                                                                                              Trichosanthes sp. Bac Kan 8-98.
Eukaryota; Viridiplantae; Strep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY EMBL; AF367252; AAK52960.1; -. Interpro; IPR001574; RIP. Pfam; PF00101; RID; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yuan H., Wang L., Wang Y., An C., Chen Z.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
                                                                                                                                                                                   NCBI_TaxID=118182;
                                                                                                                                                                                                                                                                             Trichobakin
                                                                                                                                                                                                                                                                                                                                                          Q9LRE3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Trichosanthes kirilowii (Mongolian snake-gourd).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel. 01-MAR-2003 (TrEMBLrel. Trichosanthin precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hydrolase; Signal; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                              SIMILARITY: BELONGS TO TE; AB039324; BAA92530.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIFIC ADENOSINE ON THE 28S RRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188
                                                                                                                                                                                                                                                                                                                                                                                                                                   194
                 P09989; 1MRJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82 TISVAIDVTNVYIMGYRAGDTSYFF---NEASATEAAKYVFKDSMRKITLPYSGNYERLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                   Chi, Nguyen Thuy Ha, Le Tran Binh;
DNA Clone for mature typ-1 ribosom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MRTRI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAAGKIRENIPLGLPALDSAITTLFYYNAN-----SAASALMYLIQSTSEAARYKFIEQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSFRLSGATSSSYGVFISNLRKALPNERKL-YDIPLL--RSSLPGSQRYALIHLTNYADE
                                                                                                                                                                                                                                                                                                                                                                                                                                   IGKRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL
   IPR001574; RIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         289 AA;
                                                                                                                                                                                                                                                                      (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 22, Last annotation update)
(EC 3.2.2.22) (rRNA N-glycosidase) (Fragment).
                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cucurbitales; Cucurbitaceae; Trichosanthes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       270 T
31706 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.3%; Score 340; DB 10; 39.5%; Pred. No. 6.8e-24;
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23,
(EC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
3.2.2.22) (rRNA N-glycosidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TRICHOSANTHIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A6D5602549CA5657 CRC64;
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                                                                                                                                                                                                                                                                                                                                                       247
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                                                                        N-GLYCOSIDIC BOND AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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Q41216
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                                                                                                            Query Match
Best Local S
Matches 73
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 22, Last annotation update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Trichosanthin (EC 3.2.2.22) (TRNA N-glycosidase).
TRICHOSANTHIN, TCS.
Trichosanthes kirilowii (Mongolian snake-gourd).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO EMBL; S70176; AAB31048.1; HSSP; P0989; 1MRJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER
                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                PROSITE; PS00275; SHIGA_RICIN; Hydrolase; Toxin.
                                                                                                                                                                                                                         InterPro; IPR001574; RIP.
Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q41216
                                                                                                                                                                                                            PRINTS; PR00396; SHIGARICIN
                                                                                                                                                                                                                                                                                                                                                  Zheng H., Wang B.,
                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94271613; PubMed=8003348;
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN;
                                                                                                                                                                                                                                                                                                                       [Cloning and DNA sequencing of the Chuan Hsueh Pao 21:42-51(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT SPECIFIC ADENOSINE ON THE 28S RRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59
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                                                                                                                            Similarity
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TISVAIDVTSVYIMGYRAGDTSYFF---NEASATEAAKYVFKDAMRKVTLPYSGNYERLQ
                        SYTLALDYTNAYVYGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE
                                                                              INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL 68
                                                      VSFRLSGATSSSYGVFISNLRKALPNERKL-YDIPLL--RSSLPGSQRYALVHLTNYADE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MRTRI 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IAAGKIRENIPLGLPALDSAITTLFYYNAN-----SAASALMVLIQSTSEAARYKFIEQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISVAIDVTNVYVMGYRAGDTSYFF---NEASATEAAKYVFKDAKRKVTLPYSGNYERLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSFRLSGATSSSYGVFISNLRKALPYERKL-YDIPLL--RSTLPGSQRYALIHLTNYADE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL
                                                                                                                                                                   289 AA; 31650 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                247 AA;
                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                  Shaw P., Yeung
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                                                                                                             46;
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                                                                                                            Pred. No. 1.1
5; Mismatches
                                                                                                                         Score 338;
Pred. No. 1
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                                                                                                                                                                   286AC14D48BCA175 CRC64;
                                                                                                                                                                                                                                                                              RIBOSOME - INACTIVATING
                                                                                                                                                                                                                                                                                                                                                    Ξ.
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                                                                                                                                                                                                                                                                                                                                 gene encoding trichosanthin].";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               289
                                                                                                                         DB 10;
l.1e-23;
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                                                                                                                                    Length 289;
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RESULT 12
Q3876
ID Q3876
AC Q3876
DT Q3876
DT Q1-NC
DT Q1-NC
DT Q1-NC
DT Q1-NC
DT Abru
OC Euka
OC Speka
OC GC
RT SEQ
RC TIS
RN MCB:
RN MCB:
RN MCB:
RT Chi
RT Chi
RT Chi
CC CC
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Best Local
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Q38760; PRELIMINARY; PRT; 232 AM.
Q38760; Q1-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-NOV-1998 (TrEMBLrel. 19, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Abrin-E (RRNA N-glycosidase) (EC 3.2.2.22) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideursids_1; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PRO0396; SHIGARICIN.

PRINTS; PRO0396; SHIGA_RICIN; 1.

PROSITE; PS00275; SHIGA_RICIN; 1.

Hydrolase; Glycosidase; Toxin; Repeat; Glycoprotein; Lectin.

Hydrolase; Glycosidase; Toxin; Repeat; Glycoprotein; Lectin.

CHAIN 1 252 ABRIN E, A CHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X54872; CAA38654.1;
HSSP; P11140; LABR.
InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chains."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=91201329; PubMed=2016300;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT (
SPECIFIC ADENOSINE ON THE 28S RRNA.
SUBUNIT: DISTULFIDE-LINKED DIMER OF A AND B CHAINS.
DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN
CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
SYMILARTIY: TO OTHER BACTERIAL AND PLANTS RIBOSOME-INACTIVATING
PROTEINS. BELONGS TO TYPE 2 RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNITS BY REMOVING ADENINE POSITION 4,324 OF 28 S RRNA. ABRIN-A IS MORE TOXIC THAN RICIN.
FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRECEDES ENDOCYTOSIS.
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       189
                                                                         120 WAHQTREQISLGLQALTHAIS---FLRSGASNDEEKARTLIVIIQMASEAARYRYISNRV
                                                                                                                                        129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PF00161; RIP;
                                                                                                                                                                                                       64 SIEVGIDVTNAYVVAYRAGSQSYFL----RDAPASASTYLFTGTQ-RYSLRFDGSYGDLER 119
                                                                                                                                                                                                                                                                      69 SYTLALDYTNAYVYGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQ 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TAAGKIRENIPLGLPALDSAITTLFYYNAN----SAASALMVLIQSTSEAARYKFIEQQ 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 187
                                                                                                                                     LAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEM 188
                                                                                                                                                                                                                                                                                                                                            IKFSTEGATSQSYKQFIEALRERLRGG--LIHDIPVLRDPTTVEERNRYITVELSNSERE 63
                                                                                                                                                                                                                                                                                                                                                                                                        INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            252
252 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28309 MW; BBFC846B9E92B5DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             33.0%; Score 336.5;
44.9%; Pred. No. 1.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.2e-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10; Length 252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
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                 δÃ
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Best Local (
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sambucus nigra (European elder).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.
                                                                                                                                 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50231; RICIN_B_LECTIN; PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY EMBL; AF409135; AAL04123.1; -:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-glycosidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q945S2
                                                                             Type 2 ribosom (EC 3.2.2.22).
                                                                                                                                                                                                                                                                                    Q8GT32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00396; SHIGARICIN. SMART; SM00458; RICIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00652; Ricin_B_lectin;
Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Van Damme E.J.M.;
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              Sambucus nigra (European elder).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                     Q8GT32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   177
                                                                                                                2 ribosome-inactivating protein nigrin 1 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184
                                                                                                                                                                                                                                                                                                                                                                                                                                                     195 IEQEVRRSLQ 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6 YPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IEGEMRTRIR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNLETAANTRRESIELGPSPLDGAITSLYHGD----SVARSLLVVIQMVSEAARFRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NGNTYTLAYDYTNLYYVAFSGNANSYFF-----KDATEVQKSNLFVGTKQN-TLSFTGNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AELSYTLALDYTNAYVVGYRAGNSAYFFHPDNQEDAEAI--THLFTDVQNRYTFAFGGNY 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YPSVSENLDGAKSATYRDFLSNLRKTVATGTYEVNGLPVLRRESEVQVKSRFVLVPLTNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         563 AA; 62242 MW; 07F7CBEDCF33BF10 CRC64;
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                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32.4%; Score 330.5; 39.5%; Pred. No. 1.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
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                                                                                                                                                                                                                                                                                           563 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.4e-22;
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61;

Indels

15;

Gaps

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RESULT PARTIES OF PART
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           뮹
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Best Local S
Matches 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q38761 PRELIMINARY; PRT; 252 AA.
Q38761; Q96234;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-CCT-2002 (TrEMBLrel. 22, Last annotation update)
Ricin A-chain type 73 (EC 3.2.2.22) (rRNA N-glycosidase)
EUR. J. BIOCHEM. 219:83-87(1994).

1 CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.

1 SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. EMBL; X54873; CAA38655.1; -.
EMBL; X56720; CAA54138.1; -.
EMBL; X76720; CAA54138.1; -.
INSEP; P11140; 1ABR.
InterPro; IPR001574; RIP.
Pfam; PF00161; RIP; 1.
PRINTS; PR00396; SHIGAARICIN.
PROSITE; PS00275; SHIGAARICIN; 1.
                                                                                                                                                                                                                                                                             MEDLINE=94139756; PubMed=8307038; Chih-Hung H., Lee M.C., Chen J.K., Lin J.Y.; Choning and expression of three abrin A-chains derived by site-specific mutagenesis in Escheric Eur. J. Biochem. 219:83-87(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Abrus precatorius (Indian licorice) (Crab's eye).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids I; Fabales; Fabaceae; Papillonoideae; Abreae; Abrus.
                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Seed
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE OF 2-252 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (OCT-1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Girbes T., Arias F.J., Antolin P.;

"Characterization and molecular cloning of Nigrin 1, a type tribosome-inactivating protein from leaves of elder (Sambucus Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AF249280; AAN86130.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Evensen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3816;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Leaf;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4202;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            G., Mathiesen A., ad (OCT-1990) to t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NGNTYTLAVDYTNLYVVAFSGNANSYFF-----KDATEVQKSNLFVGTKQN-TLSFTGNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IEGEMRTRIR 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AELSVTLALDVTNAYVVGYRAGNSAYFFHDDNQEDAEAI--THLFTDVQNRYTFAFGGNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNLETAANTRRESIELGPSPLDGAITSLYHGD-----SVARSLLVVIQMVSEAARFRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YPSVSFNLDGAKSATYRDFLSNLRKTVATGTYEVNGLPVLRRESEVQVKSRFVLVPLTNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IEQEVRRSLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ından A.;
EMBL/GenBank/DDBJ databases.
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Pred. No. 1.4
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Escherichia coli.";
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Best Local (
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                       187
                                            118
                                                                  127
175 RVRVSIQ
                                                                                   64 SIEVGIDVTNAYVVAYRAGTQSYFLRDAPSSASD-----YLFTGT-DQHSLPFYGTYGDL
                                                                                                              69
                                                                                                                                   6
                                                                                                                                                                               80;
                                                                                                                                                     9 INFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILVELSNHAEL
                                                                                                                                                                                           Similarity
                                                     EQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEG
                                                                                                                                EMRTRIR 193
                                                                                                    SVTLALDVTNAYVVGYRAGNSAYFFH--PDNQEDAEAITHLFTDVQNRYTFAFGGNYDRL
                                           ERWAHQSRQQIPLGLQALTHGIS---FFRSGGNDNEEKARTLIVIIQMVAEAARFRYISN
                                                                                                                                                                                                                           252
252 AA;
                                                                                                                                                                               Conservative
                                                                                                                                                                                                                          28229 MW;
                                                                                                                                                                                        32.3%; Score 329.5;
42.8%; Pred. No. 5.
                                                                                                                                                                               28;
                                                                                                                                                                                                                         187B8B4E134AECE5 CRC64;
                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                  DB 10; Length 252;
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                                                                                                                                                                            Gaps
                                                               186
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Search completed: September 16, Job time: 31.5828 secs

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Maximum DB seq length: 200000000
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                  A_Geneseq_19Jun03:*

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1 IFPKQYPIINFTTA
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

44 45	42	4 O	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10
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289 289 289	289	289	267	267	248	248	247	247	280	534	540	540	267	267	332	534	267	267	574	574	268	565	200	576	576	576	576	576	576	565	565	565
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AAR32986 AAR55129 AAW10468	AAR29272	AAR07514	AAW21703	AAW25140	AAR25573	AAR07518	AAY69048	AAR67359	AAP95648	AAP70324	AAW21706	AAW25143	AAR32430	AAR74176	AAR06554	AAR39571	AAB19265	AAR30722	AAP94793	AAP70325	AAR39570	AAP60240	AAP80164	AAG78302	AAG78301	AAY78592	AAY55892	AAW25787	AAP70326	AAG78304	AAG78300	AAP50166
Encodes chinese cu Alpha-trichosanthi Chinese cucumber a	Trichosanthin prot		H	Trichosanthin (a r	Mature alpha-Trich	Synthetic alpha-tr	Amino acid sequenc	Trichosanthin anti	Ricin agglutinin A	Sequence of Ricin	⊂	r oil	P	A chain	gene	Sequence of G-FIT.		Ricin A from pICI1	uenc	of R			etic	bean	bean prepr	Ricinus communis r	Castor bean ricin		Sequence of Ricinu	O.	bean	Sequence of prepro

## ALIGNMENTS

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RESULT 1
AAR37290
                                                                                                                                                                                     25-MAR-2003
09-JAN-2003
13-SEP-1993
       WPI; 1993-167617/20
                                                                                                                                          Type II ribosome-inactivating protein; type II RIP; gelonin; momordin; immunoconjugate; autoimmune disease; cell killing; toxin.
                                                                                                                                                                                                                                     AAR37290 standard; protein; 267 AA
                      Berhard SL, Better MD,
                                      (XOMA ) XOMA CORP.
                                                      04-NOV-1991;
19-JUN-1992;
                                                                              04-NOV-1992;
                                                                                              13-MAY-1993.
                                                                                                             W09309130-A1.
                                                                                                                              Unidentified
                                                                                                                                                                     Ricin A chain.
                                                                                                                                                                                                                     AAR37290;
                                                                                                                                                                                    (updated)
(updated)
(first entry)
                                                      910S-0787567
920S-0901707
                                                                              92WO-US09487.
                      Carroll SF,
                      Lane
                      JA,
                      Lei SP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention covers analogues of Type I RIPs. Ricin is a Type II RIPs whose A chain is homologous to plant type I RIPs. The analogues of the invention have a cysteine available for intermolecular disulphide bonding at an amino acid position corresp. to a position not naturally available for bonding; the cys residue is located in the C-terminal region of the analogue between a position corresp. to amino acid 251 and the C-terminus of ricin A chain. The analogues are pref. joined via a disulphide linkage to a molecule which specifically binds to a target cell, e.g. an antibody fragment. (Updated on 09-JAN-2003 to add missing OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Analogues of type I ribosome inactivating protein - useful as cytotoxic agents, immuno toxins for treating auto immune diseases, cancer, graft versus host disease and selective cell killing in=vi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 92; 163pp; English.
 Polynucleotide(s) encoding type I ribosome-inactivating
                            WPI; 1995-006804/01
                                                       Better MD,
                                                                               (XOMA ) XOMA CORP.
                                                                                                                                     12-MAY-1994;
                                                                                                                                                                                          WO9426910-A1
                                                                                                                                                                                                                     Ricinus communis.
                                                                                                                                                                                                                                              graft-versus-host
                                                                                                                                                                                                                                                          Ricin A chain; RTA; ribosome-inactivating proteins; RIPs; cytotoxic therapeutic agents; autoimmune disease; cancer;
                                                                                                                                                                                                                                                                                                 Ricin A-chain
                                                                                                                                                                                                                                                                                                                              25-MAR-2003
27-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                     AAR63902;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                24-NOV-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 GNYDRLEQLAGNLRENTELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 188;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FOYIEGEMRTRIRYNRRS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      267 AA;
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                                                     Carroll
                                                                                                                                                                                                                                                                                                                            (updated)
(first entry)
                                                                                                                                                                                                                                                                                                   (RTA).
                                                                                                           93US-0064691
                                                                                                                                     94WO-US05348
                                                       SS,
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                                                       Studnicka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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Pred. No. 9.2e-94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                       GM,
                                                     Carroll
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RESULT 3
AAW25136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR63902 is the ricin A chain gene product, it is analogous to the ribosome-inactivating proteins (RIPs) described in AAR63903-R63911. RIPs are the key components of cytotoxic therapeutic agents (CTAS), which include gene fusion products and immunoconjugates. CTAS may be used to selectively eliminate any cell type to which a RIP component is targetted, by the specific binding capacity of the second component of the agent. They can be used in the treatment of diseases where the elimination of a particular cell type is desired, such as autoimmune disease, cancer and graft-versus-host
                            09-DEC-1992;
11-JUN-1990;
26-JAN-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            \cdot which are suitable for use as components of cytotoxic therapeutic agents.
                                                                                                                                                                                                                                                                     Maize; proRIP; ribosome inactivating protein; alpha; beta subunit; internal linker; Barley Translation Inhibitor; Trichosanthin; Ricin A-chain; Abrin-A A-chain; Saporin; SLT-1; Luffin A; MAP; Ricinus communis agglutinin; Momordin; PAP-S; Luffin-B; Dianthin 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                25-MAR-2003
02-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW25136 standard;
                                                                                                     07-JUN-1995;
                                                                                                                                     08-JUL-1997
                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                          therapeutic toxin; tumour cell targeted; protein synthesis inhibitor; post-translational modification; cancer; neoplasia; HIV: AIDS;
                                                                                                                                                                                                                                                          therapeutic
                                                                                                                                                                                                                                                                                                                                                   Ricin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                            human immunodeficiency virus; acquired immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188;
                                                                                                                                                                                                                                                                                                                                                  A-chain ribosome inhibitory protein inactive precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 IFPKQYPIINETTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FQYIEGEMRTRIRYNRRS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FQYIEGEMRTRIRYNRRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       267 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                (updated)
(first entry)
                            92US-0987927.
90US-0535636.
95US-0378761.
95US-0485286.
                                                                                                        95US-0485286
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 951; DB 16;
Pred. No. 9.2e-94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          À
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                               deficiency syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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60

120 110

(DOWC ) DOWELANCO

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                                                                                                                                                                                                                                                                                             RESULT
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       toxins targeted to specific cells such as tumour cells via the attachment of a targeting polypeptide, e.g. a monoclonal antibody. A further use is in HIV therapy (see Us4869903). There is interest in expressing RIP recombinantly in host eukaryotic cells, because of the capacity to provide correct post-translational processing. However, RIPs effectively inhibit protein synthesis in eukaryotic cells resulting in cell death. Since the inactive RIP proteins are not cytotoxic to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW25136 represents a Ricin A-chain ribosome inhibitory protein (RIP) which was engineered to contain a selectively removable internal peptide linker sequence separating the alpha and beta units of the RIP. When separated the two units regain activity and are capable of inactivating eukaryotic ribosomes and hence preventing protein production. Many different RIPs may be produced with an internal linker including maize RIP, Trichosanthin, Ricin A-chain, Abrin-A A-chain and
                                                                         pro-Ribosome Inactivating Protein; proRIP; peptide linker; cancer; inactivation; eukaryottc ribosome; alpha fragment; beta fragment; inhibitor; protein synthesis; N-glycosidase; glycosidio bond; liver; rat; ribosommal 28S RNA; cellular proliferation; HIV-infected T cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       eukaryotic cells, they can be recombinantly expressed in such cells and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding pro-ribosome inactivating proteins - inactive precursors of ribosome inactivating proteins; can be expressed eukaryotic cells without causing cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 неу
                                              Ricinus
                                                                                                                                                     Ricin A-chain RIP
                                                                                                                                                                                    25-MAR-2003
26-SEP-1997
                                                                                                                                                                                                                                AAW21699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Saporin.
                                                                                                                                                                                                                                                               AAW21699 standard;
                                                                                                                                                                                                                                                                                                                                                                                                     145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51
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                                              communis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Column
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The RIPs can be used in the construction of therapeutic
                                                                                                                                                                                                                                                                                                                                                                     FQYIEGEMRTRIRYNRRS
                                                                                                                                                                                                                                                                                                                                                                                                                     GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                        FOYIEGEMRTRIRYNRRS
                                                                                                                                                                                                                                                                                                                                                                                                   GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Morgan AER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 290 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-2003 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                 (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to active RIP proteins.
-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91-94; 186pp; English.
   Location/Qualifiers 152..162
                                                                                                                                                                                                                                                               Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Walsh TA;
                                                                                                                                                                                                                                                                                                                                          222
                                                                                                                                                                                                                                                                                                                                                                        188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                               290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 951; DB 1:
Pred. No. le-93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 18; Length 290;
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RESULT 5
AAP70097
ID AAP7
XX
AC AAP7
XX
AC AAP7
XX
DT 09-A
XX
Rici
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AAP70097; 09-APR-1991

(first entry)

AAP70097 standard; protein;

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Matches
                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                    Proteins (RIP's), which may be used in the construction of the proteins (RIP's), which may be used in the construction of the invention. The protein has a selectively removable, internal peptide linker. The precursor sequence is incapable of inactivating eukaryotic ribosomes, but can be converted by removal of the linker into a protein having alpha and beta fragments and being capable of inactivating eukaryotic ribosomes. RIPs are potent inhibitors of eukaryotic protein synthesis. They possess a highly specific N-glycosidase activity which cleaves the glycosidic bond of adenine 4324 of rat liver ribosomal 28S RNA. RIP's selectively inhibit cellular proliferation of cells, e.g. cancer cells and HIV-infected T cells. The inactive proRIP proteins make it possible to provide protein synthesis inhibitors with uses in practical and improved ways not before possible. The RIP can be used to make cytotoxic conjugates.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inactive chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequences given in AAW21698-710 represent Ribosome Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-DEC-1992;
11-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US5635384-A.
                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  internal linker sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-309831/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hey TD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-JUN-1997
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                                                                                                                                                                                                                                                                          Local
                                                               145
                                                                                               111
205
                               171
                                                                                                                                                                                                                                                           188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Column 91-94; 121pp; English.
                                                                                                                               85
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                                                                                                                                                                                            25
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                                                                                                                                                                                                                                                                          Similarity
                                                                              GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
                                                                                                                                                                                                              IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              precursor of maize ribosome-inactivating protein - also ribosome-inactivating protein precursors containing
FQYIEGEMRTRIRYNRRS
                               FQYIEGEMRTRIRYNRRS 188
                                                              GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
                                                                                                                               ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                                                                                                             ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                                                                                                                                             IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Morgan AER,
                                                                                                                                                                                                                                                                                                                           290
                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92US-0987927.
90US-0535636.
95US-0378761.
                                                                                                                                                                                                                                                                                                                           AΑ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Position of possible insertion of internal
    peptide linker sequence"
                                                                                                                                                                                                                                                                         98.4%;
94.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Walsh TA;
                                                                                                                                                                                                                                                                          Score 951; DB 1
Pred. No. 1e-93;
                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                        Length 290;
                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                           10;
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                                                                                                                               144
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RESULT 6
AAP70838
ID AAP7
XX AAP7
AC AAP7
XX 25-M
DT 18-F
XX Sequ
DE Sequ
DE A pr
XW Lect
KW Lect
KW Plan
XX Rici
XX Rici
XX Regi
FT Regi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ricin A may be produced in a form which lacks an N-terminal Metusing Met-aminopeptidase from {\tt E.coli.}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-terminal methionine free proteins prodn. - by using host transformed with vector to express a methionine-amino-peptidase % \left( 1\right) =\left\{ 1\right\} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1987-110172/16.
N-PSDB; AAN70152.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-MAY-1986;
20-SEP-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli.
                                   Region
                                                                                         Ricinus communis
                                                                                                                            plant toxin.
                                                                                                                                           Lectin; toxin
                                                                                                                                                                                A protein encoded
                                                                                                                                                                                                 Sequence of Ricinus communis castor beans ricin toxin (RT or ricin)
                                                                                                                                                                                                                                    18-FEB-1991
                                                                                                                                                                                                                                                     25-MAR-2003
                                                                                                                                                                                                                                                                                                                          AAP70838 standard; protein; 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig. 4; 20pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Benbassat A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CETU ) CETUS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-SEP-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-APR-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EP219237-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ricin A; Met-aminopeptidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188;
                                                                                                                                                                                                                                                                                                                                                                                                                 216
                                                                                                                                                                                                                                                                                                                                                                                                                                  171 FQYIEGEMRTRIRYNRRS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFFPDNQEDAEAITHLFTDVQNRYTFAFG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILV 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
                                                                                                                                                                                                                                                                                                                                                                                                                 FQYIEGEMRTRIRYNRRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                 (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bauer KA,
                                                                                                                                             protein; cytotoxic; cytostatic; castor bean,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86US-0860330
85US-0778414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86EP-0307242
   /note="Leader"
33..302
                                                     Location/Qualifiers
                                                                                                                                                                              by pRA123.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 951; DB 8;
Pred. No. 1.2e-93;
0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ŝ
                                                                                                                                                                                                                                                                                                                            A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 332;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155
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                                                                                                          RESULT 7
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                                                                                                                                                                                                                                                                                                                                                           QΥ
                                                                                                                                                                                                                                                                                                                                                                                               Вþ
                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The full-length sequences encoding ricin A (AAN70520), ricin D (AN70525), putative ricin E (AN70526) and RCA (AN70524) in precursor CC form were obtd. using messenger RNA to obtain a cDNA library, and CC then probing the library to retrieve the desired cDNA library, and CC then probing the library to retrieve the desired cDNA library, and CC library was probed using the 35-mer given in AN70514. Figure 4 (see AN70520, AAN70521, AN70522) shows the nucleotide sequences of three CC plasmids contg. cDNA inserts obtd. by probing a cDNA library for sequences encoding ricin B using the probe in AN70517. The cDNA linserts can be placed into expression vectors. Site-directed contagenesis may be used to place an ATG start codon and a HindIII coming sequences of the inserts can be ligated into expression coding sequences of the inserts can be ligated into expression coding sequences of the inserts can be ligated into expression coding sequences of the inserts can be ligated into expression coding sequences of the inserts can be ligated into expression coding sequences of the inserts can be ligated into expression coding sequences of the inserts can be ligated into expression coding sequences of the inserts can be ligated into expression coding sequences of the inserts can be ligated into expression coding sequences of the inserts can be ligated into expression coding sequences of the inserts can be ligated into expression coding sequences of the inserts can be ligated into expression coding sequences of the inserts can be ligated into expression coding sequences of the code of the mature protein (see AN70518). The coding sequences of the inserts can be ligated into expression coding sequences of the inserts can be ligated into expression code of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
   25-MAR-2003
31-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Region
                                                         AAP95639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 1; 112pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New non-glycosylated ricin precursor and toxin etc. - are prepd
by recombinant DNA procedures with specific isolation steps for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAN70519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1987-265177/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13-NOV-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-SEP-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP237676-A.
                                                                                           AAP95639 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 purer and soluble prods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CETU ) CETUS CORP. (CHIR ) CHIRON CORP
                                                                                                                                                                                171 FQYIEGEMRTRIRYNRRS 188
                                                                                                                                                                                                                                                                        111 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 170
                                                                                                                                                                                                                                                       156 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
                                                                                                                                                                                                                                                                                                                            96 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                                                                                                                                                                                                                                                                                              51 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188;
                                                                                                                                                                                                                                                                                                                                                                                                 36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                     1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILV 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            332 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
 (updated)
(updated)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86US-0837583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="A-chain"
315..332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="B-chain"
                                                                                             protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98.4%;
94.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 951; DB 8;
Pred. No. 1.2e-93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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10;

Gaps

95

215

13-AUG-1990

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                                                                                                  Matches
                                                                                                          Query Match
Best Local :
                                                                                                                                                                                             Plasmid RA123 (ATCC No. 39799) carries the entire coding sequence for ricin A, as well as codons for 12 AAs joining the A to the B chain Following modification for ease of manipulation the plasmid was used
                                                                                                                                                                                                                                              Recombinant vectors expressing ricin chains or diphtheria toxin -used prodn. of new immunotoxin conjugates with monoclonal antibodies, havin high cell specificity and good extracellular stability.
                                                                                                                                  Sequence
                                                                                                                                                                                                                                Disclosure; Fig 14; 54pp; English.
                                                                                                                                                                                                                                                                                         WPI; 1989-286959/40.
                                                                                                                                                                                                                                                                                                                  Gelfand
                                                                                                                                               (Updated on 31-OCT-2002 to add missing OS field.)
(Updated on 25-MAR-2003 to correct pr field.)
(Updated on 25-MAR-2003 to correct pr field.)
(Updated on 25-MAR-2003 to correct Pr field.)
                                                                                                                                                                                        construct expression vectors which express the conjugates in
                                                                                                                                                                                                                                                                                                         Piatak
                                                                                                                                                                                                                                                                                                                                                                08-FEB-1984;
09-FEB-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                EP335476-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                  nost cells.
                                                                                                                                                                                                                                                                                                                                (CETU ) CETUS CORPORATION.
                                                                                                                                                                                                                                                                                                                                                 20-SEP-1984;
                                                                                                                                                                                                                                                                                                                                                                                 08-FEB-1984;
                                                                                                                                                                                                                                                                                                                                                                                                 19-JAN-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                 04-OCT-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ricinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ricin A encoded by insert from plasmid pRA123.
      111 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTOLPTLARSFIIGIQMISEAAR 170
                                                                                                  188;
                                       51 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                  36
                                                                                                                                                                                                                                                                                                          ,
M
D
                                                                              1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                  AAN91281
                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         communis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pRA123; ricin-A; ricin-B; cytotoxicity
GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
                                                              ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                                                                                 332 AA;
                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                Lawyer FC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                              84US-0578115.
84US-0578121.
84US-0578122.
84US-0578122.
84US-0648759.
84US-0653515.
                                                                                                                                                                                                                                                                                                                                                                                               89EP-0201162
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label=linker
315..332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                /label=B-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label=A-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= leader sequence
                                                                                                        98.48;
                                                                                                                                                                                                                                                                                                                Horn
                                                                                                 0,
                                                                                                        Score 951; DB 10;
Pred. No. 1.2e-93;
                                                                                                                                                                                                                                                                                                                ģ
                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                              Greenfield L,
                                                                                                               DB 10;
                                                                                                 0
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                                                                                                              Length 332;
                                                                                                Indels
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215
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RESULT 8
AAR70827
ID AAR7
                                  Query Match
     Matches 188;
                     Best Local Similarity
                                                                                                  The immunotoxin given in AAR70827 comprises the heavy and light chain variable regions of anti-lens epithelium IgG3 MAb 4197% linked to ricin-A and a hexa-histidine tag. The DNA construct encoding the immunotoxin was expressed from pHB19 in E. coli. (Updated on 25-MAR-2003 to correct PN field.)
                                                                      Sequence
                                                                                                                                                                                                                                         New single chain immuno:toxin - binds specifically to epithelial cells, for inhibiting development of sec. cataracts after extra:capsular cataract extraction.
                                                                                                                                                                                                         Disclosure; Fig.4; 68pp;
                                                                                                                                                                                                                                                                                                                 N-PSDB; AAQ85386.
                                                                                                                                                                                                                                                                                                                                                                    Gould RM,
                                                                                                                                                                                                                                                                                                                                WPI; 1995-082036/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                      02-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUL-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-MAR-2003
31-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                  (HOUS-) HOUSTON BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9503828-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      рнв19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunotoxin; heavy chain; light chain; variable region; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-cataract
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR70827 standard; Protein; 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cin-A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   171 FQYIEGEMRTRIRYNRRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    216 FQYIEGEMRTRIRYNRRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4197X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytostatic; cataract; lens opa
197X; monoclonal antibody; MAb.
                                                                                                                                                                                                                                                                                                                                                                  Kelleher PJ,
                                                                       554
     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (updated)
(first entry)
                                                                       AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunotoxin
                                                                                                                                                                                                                                                                                                                                                                                                                                    930S-0101329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94WO-US07919
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Sig_peptide
/note= "phoA signal
28..145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            549..554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= LIGHT
/note= "MAb 419X light chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "hexa-histidine tail"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= RICIN-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= LINKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "MAb 4197X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= HEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'label=
                   98.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .166
                                                                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                                                                                Wallace TL,
Score 951; DB 16;
Pred. No. 2.5e-93;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      233
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lens opacification; epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             heavy chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence"
                                                                                                                                                                                                                                                                                                                                                                  Wood
   0;
                                Length 554;
   Indels
 10;
 Gaps
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RESULT 9
AAP90079
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                                            Best Loc
Matches
                                                           Query Match
                                                                                                                                                                                                                                                                                                                            Ricin D; Ricinus communis; caster beans; Zanibariensis variety; modified; lectin binding removed; reduced cell binding
                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                       AAP90079;
                                                                                                                                                                                                                                                                                                                                                                                                     AAP90079 standard;
                                                                                                                                                                                                                                                                                01-JUN-1989
                                                                                                                                                                                                                                                                                                W08904839-A.
                                                                                                                                                                                                                                                                                                             Ricinus communis (caster beans).
                                                                                                                                                                                                                                                                                                                                                   Ricin
                                                                                                                                                                                                                                                                                                                                                                        25-MAR-2003
                                                                                                             Ricin D (see corresp. AAN90068) found on the EcoRI-HindIII fragment of DNA from Ricinu communis, Zanibariensis variety. Patent discloses many modifications of ricin in which the lectin binding function of the B chain is diminished or removed, and conjugation
                                                                                                                                                                 Modified ricin molecules and toxin conjugates - in which the lectin binding function of the B chain is removed or diminished to reduce cell binding.
                                                                                                                                                                                                                                                                  23-NOV-1988;
                                                                                       to toxins to eliminate cell binding. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                     Brown EL,
                                                                                                                                                                                                                                    (GEMY ) GENETICS INST INC
                                                                                                                                                                                                                                                   24-NOV-1987;
                                                                         Sequence
                                                                                                                                                   Disclosure; fig 1; 51pp; English.
                                                    Loca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      338
                                                                                                                                                                                                                                                                                                                                                                                                                                           458
                                                                                                                                                                                                                                                                                                                                                                                                                                                         171
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                                                                                                                                                                                                1989-178366/24.
DB; AAN90068.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1
51 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 110
                36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                           FQYIEGEMRTRIRYNRRS 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                          FQYIEGEMRTRIRYNRRS 188
               IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILV 50
                                                                                                                                                                                                                     Jones S;
                                                                          562 AA;
                                                                                                                                                                                                                                                                                                                                                                 (updated)
(first entry)
                                             Conservative
                                                                                                                                                                                                                                                    87US-0124735
                                                                                                                                                                                                                                                                   88WO-US04238
                                                                                                                                                                                                                                                                                                                                                                                                      protein; 562 AA
                                                    98.4%;
                                              0,
                                             Score 951; DB 10;
Pred. No. 2.5e-93;
0; Mismatches 0;
                                               0;
                                                             Length 562;
                                                Indels
                                                10;
                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    덩
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
                                                                                                                                                                                                                                                                                                                                                       Key
                                                                                                                             WPI;
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Preproricin is the whole polypeptide encoded by AAN50202 and the DNI encoding this is claimed. Proricin is obtained from preproricin by removal of the AA leader sequence. The linker AA sequence which is present in the precursor polypeptide is enzymatically removed in the cell to separate the A and B chains, which are joined by a disulphide bridge during the formation of the ricin molecule itself. This linker region as well as the presumptive amino terminal leader or signal sequence are not present in the sequences already published by Funatsu et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAP50166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAP50166 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ricinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Toxin; anti-tumour therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence of preproricin encoded by pRCL617.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP145111-A.
                                                                                                                                                                                                                                                              New DNA sequences coding for ricin type plant toxin mutants, and modified vectors and host microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JUL-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13-MAR-1984;
15-JUL-1983;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-JUL-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JUN-1985
                                                                                                                                                                                                                    Disclosure; Page 30-30c; 40pp; English.
                                                                                                                                                                                                                                                                                                                                N-PSDB; AAN50202.
                                                                                                                                                                                                                                                                                                                                                                                            Lord JM,
                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYWA-) UNIV WARWICK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171 FQYIEGEMRTRIRYNRRS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1985-148040/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FOYIEGEMRTRIRYNRRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFITCIQMISEAAR
                                                                                                                                                                                                                                                                                                                                                                                            Roberts LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84GB-0006569.
83GB-0019265.
83CH-0019265.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84EP-0304801.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= N-linked glycosylation 398..400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= N-linked glycosylation 260..262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    438..440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= links the C-terminus of the A chain and the N-terminus of the B chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= N-linked glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'label= N-linked glycosylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233
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RESULT 11
AAG78300
ID AAG78300
AC AAG78
XX Castc
XX Castc
XX Castc
XX Pept
FT Pept
FT Prot
FT Pept
FT Pot
FT Pept
FT Pot

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
       Disclosure; Page 47-50; 66pp; English
                                                  virus infection.
                                                       Novel composition comprising toxin e.g., ricin based antiviral compound useful for treating viral infections such as human immunodeficiency
                                                                                                                     WPI; 2001-581908/65.
N-PSDB; AAI64137.
                                                                                                                                                                             Keener WK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Castor bean plant; preproricin; ricin; A chain; B chain; human immunodeficiency virus infection; HIV; toxin; antiviral agent; retroviral infection; anti-HIV; virucide activity; viral protease.
                                                                                                                                                                                                                                                  16-FEB-2000; 2000US-0182759
                                                                                                                                                                                                                                                                                     15-FEB-2001; 2001WO-US05282
                                                                                                                                                                                                                                                                                                                                                                WO200160393-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ricinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Castor bean
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG78300 standard; Protein; 565
                                                                                                                                                                                                              (BECH-) BECHTEL BWXT IDAHO LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              communis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIOMISEAAR 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FQYIEGEMRTRIRYNRRS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FOYIEGEMRTRIRYNRRS 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHDIPVLPNRVGLPINQRFILV
                                                                                                                                                                             Ward TE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                565 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preproricin protein (SEQ ID 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Linker_peptide
/note= "Cleaved during activation of ricin"
303..565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "N-glycosidase"
291..302
                                                                                                                                                                                                                                                                                                                                                                                                   /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Ricin_A_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= Signal peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                 'label= Ricin_B_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98.4%;
94.9%;
                                                                                                                                                                                                                                                                                                                                                                                         "Galactose/N-acetylgalactosamine-binding lectin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 951; DB 6;
Pred. No. 2.5e-93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144
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     δõ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ş
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ДЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG78304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
Cleavage-site
                                      Peptide
                                                                                              Protein
                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                           Peptide
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Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Castor bean plant; preproricin; ricin; A chain; B chain; human immunodeficiency virus infection; HIV; toxin; antiviral agent; retroviral infection; anti-HIV; virucide; viral protease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Modified castor bean preproricin (SEQ ID 10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG78304 standard; Protein; 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention is useful for treating human immunodeficiency virus infection and other viral infections, especially retroviral infections. The antiviral agent is activated in viral particles or early-stage infected cells, killing the cells upon infection and effectively preventing the integration of the viral genome into the host genome thereby preventing the latency/rebound problem. The agent enters all HIV susceptible cells, and not just cells known to act as host cells for the virus. The antiviral agent remains inert in a cell until degraded in it, unless the cell is infected with the virus, where the viral protease activates it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG78304;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activities. Its mechanism of action is through inactivation of cellular ribosomes and enhancement of binding of the antiviral agent to galactose residues on cell surfaces, and its cellular internalisation. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence relates to preproricin protein encoded by the DNA sequence given in AAI64137. The invention relates to a novel toxin (e.g., ricin) based antiviral agent which is toxic to virus-infected cells, but non-toxic to uninfected cells. The invention has anti-HIV and virucide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIIGIQMISEAAR 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            171 FOYIEGEMRTRIRYNRRS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHDIPVLFNRVGLFINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILV 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FOYIEGEMRTRIRYNRRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ricinus communis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   565 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
/label= I
296..297
                                                                 /note= "1
292..303
                                                                                                                                                   /label= Proricin
/label= Proricin consists of the ricin A chain, a linker
/note= "Proricin consists of the ricin A chain, a linker
peptide, and the ricin B chain. Proricin is
proteolytically cleaved between the A chain and
the linker to yield mature ricin"
                                                                                                                          /label=
                                                                                                                                                                                                                                                                                                                                  /label= Signal_peptide 25..565
                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunodeficiency virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98.4%;
                                                                                       "N-glycosidase"
                                  Linker_peptide
                                                                                                                      Ricin_A_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 951; DB 22;
Pred. No. 2.5e-93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84.
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                                                                                                                                                                                                                                                                                  QΥ
                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                              Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence relates to the amino acid sequence of a modified preproricin CC protein encoded by AAI64145. The invention relates to a novel toxin CC (e.g. ricin) based antiviral agent which is toxic to virus-infected CC cells, but non-toxic to uninfected cells. The invention has anti-HIV and CC virucide activities. The agent is able to enter all HIV susceptible CC cells, and not just cells known to act as host cells for the virus. The CC ells, and not just cells known to act as host cells for the virus. The CC with the HIV virus, where the viral protease activates it. Ricin's CC mechanism of action is through inactivation of cellular ribosomes and CC enhancement of binding of the antiviral agent to galactose residues on CC cell surfaces, and its cellular internalisation. The invention is useful CC infections, especially retroviral infections. The antiviral agent is CC activated in viral particles or early-stage infected cells, killing the CC cells upon infection and effectively preventing the integration of the CC viral mome into the host genome thereby preventing the latency/rebound
                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel composition comprising toxin e.g., ricin based antiviral compound useful for treating viral infections such as human immunodeficiency
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-FEB-2001; 2001WO-US05282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200160393-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAI64145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Keener WK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BECH-) BECHTEL BWXT IDAHO LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-FEB-2000; 2000US-0182759.
               AAP70326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 59-63; 66pp; English.
                                             AAP70326 standard; Protein; 576 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-581908/65
                                                                                                                             205
                                                                                                                                          171 FQYIEGEMRTRIRYNRRS 188
                                                                                                                                                                                         145
                                                                                                                                                                                                        111 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 170
                                                                                                                                                                                                                                                       85
                                                                                                                                                                                                                                                                                     51
                                                                                                                                                                                                                                                                                                                                                                                    188;
                                                                                                                                                                                                                                                                                                                     25
                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                     ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                                                                                                                                                                                                       ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                                                                                                                                                                                                                                                                     IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                     IFPKQYPIINETTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILV
                                                                                                                                                                                         GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
                                                                                                                           FOYIEGEMETRIRYNERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ward TE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                565
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= HIV_protease_cleavage_site
304..565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= Ricin_B_chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Galactose/N-acetylgalactosamine-binding lectin"
                                                                                                                                                                                                                                                                                                                                                                                                98.4%;
94.9%;
                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                Score 951; DB 22;
Pred. No. 2.5e-93;
                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 565;
                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                    10;
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                        84
                                                                                                                                                                                                                                           밁
                                                                              Qy
                                                                                                              Db
                                                                                                                                            δÃ
                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                               Matches 188;
                                                                                                                                                                                                                                                                    for sequences encoding ricin B using the probe in AAN70517. The clinserts can be placed into expression vectors. Site-directed mutagenesis may be used to place an Ang start codon and a HindIII site at the beginning of the mature protein, (see AAN70518). The coding sequences of the inserts can be ligated into expression vectors containing the PhoA promoter-operator and leader sequence (AAN70523) and suitable retroregulators.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (CETU )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Кеу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ricinus communis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence of Ricinus communis (castor bean) Ricin toxin (RT or ricin) E precursor encoded by pRT38.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAR-2003
21-MAY-1991
                                                                                                                                                                                                                                                                                                                                                                                      The full length sequences encoding ricin A (AAN70520), ricin D (AAN70525) putative ricin E (AAN70526) and RCA (AAN70524) in precursor form were obtained, using the messenger RNA to obtain a CDNA library, and then probing the library to retrieve the desired cDNA inserts. The library was probed using the 35-mer given in AAN70514. Figure 4 (see plasmids containing cDNA inserts obtained by probing a cDNA library tor sequences encoding ricin B using the probe in AAN70517. The cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New non-glycosylated ricin precursor and toxin etc. - are post recombinant DNA procedures with specific isolation steps purer and soluble prods.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAN70526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1987-265177/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-MAR-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-NOV-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-SEP-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP237676-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plant toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lectin; toxin protein; cytotoxic; cytostatic;
                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 14(1-2); 112pp; English.
111 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
                                                                    51 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                                                                               1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILV 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHIRON CORP.
                                                IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                                                                                                                                                                                                                             576 AA;
                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        86US-0837583.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86EP-0308877.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36..302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "B-chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "leader"
                                                                                                                                                                                              98.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "A-chain"
                                                                                                                                                                               0,
                                                                                                                                                                                              Score 951; DB 8; Pred. No. 2.6e-93;
                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               castor bean;
                                                                                                                                                                                                               Length 576;
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Indels

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This polypeptide comprises the castorbean cytotoxin, ricin. DNA (see AAT91638) encoding the enzymatic A domain and a portion of the A-to-B linker peptide of ricin was used to construct a ricin-diphtheria toxin B'-interleukin-2 gene that was expressed in E. coli. The hybrid protein can be isolated and used to treat conditions involving over-production of cells bearing II2 receptors, such as certain T-cell lymphomas and organ transplant rejection crises. The hybrid inactivates ribosomes in cells bearing IL2 receptors, resulting in cessation of protein synthesis and death of target cells. Claimed hybrid proteins comprise a translocation domain and a cell binding domain from e.g. a hormone, growth factor or polypeptide toxin. The hybrid molecules can be used for the
                                                                                                                                                                                                                                                                                                                                                                                     07-JUN-1984;
25-APR-1985;
07-JUN-1985;
                                                                                                                                                                                                             New hybrid molecules for delivery of agents to cells -
binding domain of a cell binding ligand and a portion of
                                                                                                                                                                         Example 4; Fig 11A-B; 30pp; English.
                                                                                                                                                                                                   translocation domain of a protein
                                                                                                                                                                                                                                                        N-PSDB; AAT91638.
                                                                                                                                                                                                                                                                   WPI; 1997-470103/43.
                                                                                                                                                                                                                                                                                                                                                                                                               27-JUN-1991;
07-JUN-1984;
                                                                                                                                                                                                                                                                                              Murphy JR;
                                                                                                                                                                                                                                                                                                                                                  04-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-AUG-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US5668255-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ricin; cytotoxin; hybrid protein; cell delivery; cell binding ligand; translocation domain; diphtheria toxin B'; interleukin-2; T-cell lymphoma; organ rejection; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Castorbean ricin
                                                                                                                                                                                                                                                                                                                      (SERA-) SERAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ricinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25-MAR-2003
27-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW25787 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FQYIEGEMRTRIRYNRRS 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (updated)
(first entry)
                                                                                                                                                                                                                                                                                                                                                           89US-0456095
90US-0538276
                                                                                                                                                                                                                                                                                                                                                                                                             84US-0618199
                                                                                                                                                                                                                                                                                                                                                                                                                                                   93US-0102387
                                                                                                                                                                                                                                                                                                                                                93US-0102387
                                                                                                                                                                                                                                                                                                                                                                                      85US-0742554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Sig_peptide 36..302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Linker
315..576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B-domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A-domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY55892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 15
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Best Local :
                                                                                                                            25-APR-1985;
07-JUN-1985;
22-DEC-1989;
14-JUN-1990;
                                                                                                                                                                               04-AUG-1993;
07-JUN-1984;
27-JUN-1991;
                                                                                                                                                                                                                                                                                                                                   Recombinant; hybrid; binding domain; ligand; animal cell; diphtheria; translocation domain; botulinum; neurotoxin; ricin; cholera; tetanus; shiga-like toxin; pertussis; translocation; cytoplasmic membrane; HIV; cytosol; therapy; genetic deficiency disease; enzyme; co-factor; poison; adipocyte; cancer; virus; infection; antibody.
                                     N-PSDB;
                                                 WPI; 1999-632431/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     delivery of agents (e.g. therapeutic genes, toxins, detectable labels) into cells. The use of a translocation mechanism ensures that the hybrid will be effective in relatively low doses, since a high proportion of the substance of interest will be taken into the targeted cells. The hybrid molecules can be manufactured as a single hybrid recombinant protein, permitting reproducibility, consistency, and the precise control of composition. (Updated on 25-MAR-2003 to correct PF field.)
                                                                                                                                                                                                                                    07-JUN-1995;
                                                                                                   (SERA-) SERAGEN INC
                                                                                                                                                                                                                                                              12-OCT-1999
                                                                                                                                                                                                                                                                                        US5965406-A
                                                                                                                                                                                                                                                                                                               Ricinus communis.
                                                                                                                                                                                                                                                                                                                                                                                                                      Castor bean ricin toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-FEB-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY55892 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            51 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT------VLDNRVGLDINQRFILV
                                      AAZ30663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FOYIEGEMRTRIRYNRRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FOYIEGEMRTRIRYNRRS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   576 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                   93US-0102387.
84US-0618199.
91US-0722484.
85US-0726808.
                                                                                                                            90US-0538276
                                                                                                                                          89US-0456095
                                                                                                                                                      85US-0742554
                                                                                                                                                                                                                                  9505-0488246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98.48;
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Pred. No. 2
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2.6e-93;
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Recombinant DNA molecule encoding the treatment of Aids and genetic

a three part hybrid deficiency diseases

protein used

in

Example 4; Fig 11; 31pp; English.

co toxin, LT toxin, C3 toxin, shiga-like toxin, pertussis toxin and tettanus coxin, which translocate the third part of the across the cytoplasmic cc membrane into the cytosol of the cell; and (c) the third part comprises cc a polypeptide entity to be introduced into the cell, which is non-native to the naturally occurring protein of (b). This sequence represents the cc castor bean ricin toxin sequence for use in generating the hybrid of the cc invention. The hybrid molecule enables the direction of appropriate cc invention. The hybrid molecule enables the direction of appropriate cc genetic deficiency diseases. The hybrid is especially used in treating cc genetic deficiency diseases, by delivering to affected cells an enzyme cc particular enzyme or a scarce precursor or cofactor, to directions such as cell, or virus infected-cells), to counteracting viral infections such as cc liv, by introducing appropriate antibodies to viral proteins. It is also involved in the process of getting non-therapeutic substances such as defectable in the process of getting non-therapeutic substances such as defectable in the process of getting non-therapeutic substances such as defectable in the process of getting non-therapeutic substances such as defectable in the process of getting non-therapeutic substances such as defectable in the process of getting non-therapeutic substances such as The invention relates to a recombinant DNA molecule encoding a hybrid protein comprising three parts: (a) the first part comprises a portion of the binding domain of a cell-binding polypeptide ligand allowing the hybrid protein to bind to an animal cell; (b) the second part comprises a portion of a translocation domain of a naturally occurring protein selected from diphtheria toxin, botulinum neurotoxin, ricin, cholera detectable labels into cells.

Sequence 576 AA;

Matches 188; Conservative Query Match 98.4%; Best Local Similarity 94.9%; IFPKQYP1INFTTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILV 50 Score 951; DB 20; Length 576; pred. No. 2.6e-93; 0; Mismatches 0; Indels 1 10; Gaps

В Ş В 36 

망 δÃ 156 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 111 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 170

QΥ 171 FQYIEGEMRTRIRYNRRS 188 FOYIEGEMRTRIRYNRRS

Search completed: September 16, 2003, 11:45:17 Job time : 31.3059 secs

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Result
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
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                                                                                                                                                                                                                                                                                                                          No.
        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                           861.5
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966
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     Query
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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 US-08-356-786-10
US-08-318-793D-61
US-08-318-793D-61
US-09-538-873-1
US-09-538-873-1
US-08-485-286-77
US-08-488-113B-6
US-08-64-350-6
US-08-64-350-6
US-08-389-6
US-08-378-761A-74
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US-08-430-1
US-08-425-336-1
US-08-488-113B-1
US-08-488-113B-1
US-08-646-360-1
US-08-639-765-1
US-09-136-389-1
US-09-136-389-1
US-09-610-838-1
PCT-US92-094487-1
PCT-US92-094487-1
PCT-US92-094487-1
S-08-356-786-8
US-08-356-786-8
US-08-485-286-27
US-08-485-286-27
US-08-485-286-27
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                                                                                                                                         Sequence 1, Appli
Sequence 8, Appli
Sequence 27, Appl
Sequence 27, Appl
Sequence 27, Appl
                                                                                                              Patent No. 5248606
Sequence 10, Appl
Sequence 16, Appl
Sequence 61, Appl
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         1, Appli
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GENERAL INFORMATION:

APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:

Lane, Julie A. Better, Marc D. Carroll, Steve F. Bernhard, Susan L.

RESULT 1 US-07-901-70 ; Sequence 1 ; Patent No.		45	44	43	42	41	40	39	38	37	36	ω U	34	ω ω	32	31	30	29	28	
RESULT 1 US-07-901-707-1 ; Sequence 1, A ; Patent No. 53		303.5	303.5	305	305	305	305	310.5	310.5	310.5	310.5	320.5	336	336	336	336	336	336	336	
SULT 1 -07-901-707-1 Sequence 1, Application US/07901707 Patent No. 5376546		31.4	31.4	31.6	31.6	٠	31.6		•				34.8				4.	34.8		
on US/O		250	250	496	290	290	248	255	255	255	255	282	289	289	289	289	289	289	267	
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1707	ALIGNMENTS	US-08-485-286-71	US-08-378-761A-71	US-08-902-486-15	US-08-597-731-2	US-08-245-754A-2	US-08-902-486-7	PCT-US92-09487-6	US-08-425-336-6	US-07-988-430-6	US-07-901-707-6	US-08-324-301-15	US-09-726-651A-4	US-08-483-502-4	US-08-484-341-4	US-08-482-920-4	US-08-184-237-4	•	US-08-485-286-74	
		71,	71,	15	N		7,	0		6		15	4	4	4	Α.	4	4, 1	Sequence 74, Appl	

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; MOLECULE TYPE: US-07-901-707-1
                                                                                                                              TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-5750
TELEX: 25-385
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 07/787,567
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT IMPORMATION:
NAME: No. 5376546and, Greta E.
REGISTRATION NUMBER: 35,302
REGISTRATION NUMBER: 37,302
                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: AMINO ACID
                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-5750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Materials Comprising and Methods of TITLE OF INVENTION: Composition and Use for Ribosome-Inactivating Proteins NUMBER OF SEQUENCE: 57
CORRESPONDENCE ADDRESS:
                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: U: FILING DATE: 19920619 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: Two First National Plaza, 20 South Clark STREET: Street CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60603
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                protein
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Query Match

98.48;

Score 951;

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Length

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us-07-988-430-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Materials Comprising and Methods of TITLE OF INVENTION: Preparation and Use for Ribosome-Inactivating Proteins NUMBER OF SEQUENCES: 101
                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 19921209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                MOLECULE TYPE:
                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (312) 346-5750
                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lane, APPLICANT: Lei,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                               TYPE: AMINO ACID TOPOLOGY: linear
                                                                                                                                                                                                              REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
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                                                                  LENGTH:
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                                                                  267 amino acids
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                                                                                                                                           (312
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                                                                                                                                                                                                        NT INEC. 5416202and, GIGG. 35302
                                                                                                                                                                                                                                                                                                                                                                                                                                              PatentIn Release #1.0, Version #1.25
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                protein
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0; Mismatches 0;
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; MOLECULE TYPE: protein
US-08-425-336-1
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                         APPLICATION: 18-APK-1//
FILING DATE: 18-APK-1//
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/064
APPLICATION LIBER: 12-MAY-1993
                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                               APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNBY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Studnika, Gary M.
                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                             TELEFAX: Ji.,
TELEFAX: Ji.,
25-3856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Chicago
STATE: Illino:
                                                                                                                                              TELEPHONE: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                             TOPOLOGY:
                                                                              TYPE:
                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                      NAME: Meyers, Thomas REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 07/901,707 FILING DATE: 19-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                       amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E: Marshall, O'Toole, Gerstein, Murray & Borun 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.25
                                                             linear
                                                                                                                                                                            312/474-6300
                                                                                                                                                                                                                                          Thomas C.
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98.4%;
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Pred. No. 1.8e-102;
 Score 951;
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Query Match

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RESULT 4
US-08-488-113B-1
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                                       TELEX: 650 388-1248 INFORMATION FOR SEQ ID NO:
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CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
US/08/488,113B
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                       SEQUENCE CHARACTERISTICS:
                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
                                                                                                                                                          FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNicholas, Janet
                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 01 FILING DATE: 18-APR-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                     REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 11022US07/200-70.p3.C2A
                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07 FILING DATE: 19-JUN-1992
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 07 FILING DATE: 09-DEC-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 07
CLASSIFICATION:
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Carroll, Stephen F.
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US-08-477-484B-1
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                                            FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNicholas, Janet
                                                                                                                                                APPLICATION NUMBER: 1
FILING DATE: 09-DEC-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/425,336
                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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APPLICANT: Carroll, S
APPLICANT: Studnika,
                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Belannia.
                            REGISTRATION NUMBER: 32,918
                                                                                                                                FILING DATE: 19-JUN-1992
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                REFERENCE/DOCKET NUMBER:
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Carroll, Stephen F.
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INFORMATION:
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                                                                                                 US 07/787,567
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son Street, 34th floor
            11022US07/200-70.P3.C2A
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Pred. No. 1.8e-102;
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SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08646360 Patent No. 5837491 GENERAL INFORMATION:
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APPLICANT: Carroll, Stephen
APPLICANT: Studnika, Gary M.
                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                           APPLICATION NUMBER: US 07 FILING DATE: 09-DEC-1992 PRIOR APPLICATION DATA:
                                                                                                             FILING DATE: 12-MAY-1
PRIOR APPLICATION DATA:
             PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                              FILING DATE: 13-MAY-1996
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                             APPLICATION NUMBER: FILING DATE: 19-JUN
                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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APPLICATION NUMBER:
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Similarity 94.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Illinois
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                                                                                                                                  12-MAY-1993
                               19-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     173
                                                                                                                                                US 08/064,691
                                               US 07/901,707
                                                                                               US 07/988,430
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us 07/787,567
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Pred. No. 1.8e-102;
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US-08-839-765-1
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Patent No. 6146631
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ATTORNEY/AGENT INFORMATION:
NAME: MCNICHOLAS, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
                                                                                                                                                                                                           APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
TITLE OF INVENTION: Immunotoxi
TITLE OF INVENTION: Proteins
NUMBER OF SEQUENCES: 169
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
TYPE: amino acid
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                          STREET: J. Chicago
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                                                                                                                         COUNTRY:
                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFFHDDNQEDAEAITHLFTDVQNRYTFAFG 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         FQYIEGEMRTRIRYNRRS 198
                                                                                                                                                                                                                                                                                                                                                                    Application US/08839765
                                                                                                                                        Illinois
                                                                                                                                                                          E: McAndrews, Held & Malloy, Ltd. 500 West Madison Street, 34th floor
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                                                                                                                         USA
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                                                                                                                                                                                                                                                                                                                   Better, Marc D.
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                                                                                                                                                                                                                                                              Immunotoxins Comprising Ribosome-Inactivating
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pred. No. 1.8e-102;
0; Mismatches 0;
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/425,336
FILING DATE: 18-APR-1995

APPLICATION NUMBER: FILING DATE: 15-AP

15-APR-1997

US/08/839,765

PRIOR APPLICATION DATA:

FILING DATE:

12-MAY-1993

US 07/988,430

US 08/064,691

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

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US-09-136-389-1
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Best Local Similarity 94.9%;
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATE: 19-JUN-100-1000 ATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 07/
APPLICATION NUMBER: US 07/
APPLICATION NUMBER: US 07/
APPLICATION NUMBER: US 07/
                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Immunocon
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                            APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
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TELEPHONE: 312/707-8889
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ATTORNEY/AGENT INFORMATION:
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REFERENCE/DOCKET NUMBER: 11022US09/200-70.P3.C3
                                               FILING DATE:
                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: MCNicholas, Janet M. REGISTRATION NUMBER: 32,91
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E: Illinois
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 08/646,360
                                                                US/09/136,389
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Pred. No. 1.8e-102;
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
TELEFAX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 267 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                    GENERAL INFORMATION:
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                               APPLICANT: Better, Marc D.
APPLICANT: Carroll, Stephen F.
APPLICANT: Studnika, Gary M.
                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                        TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: 312/707-8889
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid TOPOLOGY: linear
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ILECOMMUNICATION -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 13-MAY APPLICATION NUMBER: FILING DATE: 12-MAY
                                                                                STATE:
                                                                                                           STREET:
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                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFFHDNQEDAEAITHLFTDVQNRYTFAFG 110
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                                                                             Chicago
: Illinois
                                                                                                                                                                                                                                                                    , Application US/09610838 6376217
                                                                                                                                                                                                                                                                                                                                                                             FQYIEGEMRTRIRYNRRS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McNicholas, Janet M.
                                                                                                                                                                                                                                                                                                                                                             FQYIEGEMRTRIRYNRRS 198
                                                                                                          500 West Madison Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                           McAndrews, Held & Malloy, Ltd.
O West Madison Street, 34th floor
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94.98;
                                                                                                                                                        Proteins: 173
                                                                                                                                                                                     Immunotoxins Comprising Ribosome-Inactivating
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OPERATING SYSTEM: PC-DOS/MS-DOS

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                                                                                                                                     RESULT 10
PCT-US92-09487-1
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                                                                                                       Sequence 1, Application:
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 0
FILING DATE: 04-NOV-1991
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PRIOR APPLICATION UNIMBER: US 07/901,707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
 TITLE OF INVENTION:
                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: 1
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FILING DATE: 12-MAY-1994
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                                                                                                                                                                                                                                                           171 FQYIEGEMRTRIRYNRRS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                               188;
                                                                                                                                                                                                   181 FQYIEGEMRTRIRYNRRS 198
                                                                                                                                                                                                                                                                                                                      61 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAFAITHLFTDVQNRYTFAFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : 267 amino acids
amino acid
                                                                                                                       Application PC/TUS9209487
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                       Lane, Julie A.
Lei, Shau-Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                312/707-8889
312/707-9155
                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                            Better, Marc D. Carroll, Stephen F.
                                                                                          Bernhard,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.4%;
Preparation
               Materials Comprising and Methods of
                                                                                          Susan L.
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Pred. No. 1.8e-102;
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   and Use
 for Ribosome-Inactivating Proteins
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RESULT 11
US-08-356-786-8
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                                                                                                                      Sequence 8, Application US/08356786 Patent No. 5877305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                    GENERAL INFORMATION:
APPLICANT: Huston
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COMPUTER READABLE FORM:
APPLICANT: Oppermann, Hermann APPLICANT: Houston, L. L. APPLICANT: Ring, David B. TITLE OF INVENTION: Biosynthe TITLE OF INVENTION: Marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Noland, Greta E.
REGISTRATION NUMBER: 35302
REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0.
FILING DATE: 19-JUN-1992
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CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                              171 FQYIEGEMRTRIRYNRRS 188
                                                                                                                                                                                                                                                                                             181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        188;
                                                                                                                                                                                                                                                                                                                                                                 61 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
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                                                                                                                                                                                                                              FQYIEGEMRTRIRYNRRS 198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                      Huston, James S.
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                   Biosynthetic Binding Protein for Cancer
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 Mismatches

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Pred. No. 1.8e-102;
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                                                                    GENERAL INFORMATION:

APPLICANT: WALSH, TERENCE A

APPLICANT: HEY, TIMOTHY D

APPLICANT: HORGAN, ALICE ER

TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE

TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING

TITLE OF INVENTION: USING
NUMBER OF SEQUENCES: 81
                                                                                                                                                                                                                                 Patent No. 5635384
                                                                                                                                                                                                                                                      Sequence 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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APPLICATION UNMER: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
REGISTRATION UNMER: 27,829
REFERENCE/DOCKET NUMBER: CRP-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy of COMPUTER: IBM PC com
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STATE:
                                ADDRESSEE: ANDREA T. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                               171 FQYIEGEMRTRIRYNRRS 188
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               INDIANAPOLIS
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                                                                                                                                                                                                                                                                                                                                            FQYIEGEMRTRIRYNRRS 199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
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US-08-485-286-27; Sequence 27, A
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Patent No. 5646026 5646119
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Best Local Similarity
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NAME: BORUCKI, ANDREA T
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 3827
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 337-4846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
            ZIP: 45268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                      APPLICANT: WALSH, TERENCE A
APPLICANT: WALSH, TENOCHY D
APPLICANT: MORGAN, ALICE ER
TITLE OF INVENTION: RIBOSOME-INACTIVATING PROTEINS, INACTIVE
TITLE OF INVENTION: PRECURSOR FORMS THEREOF, A PROCESS FOR MAKING A METHOD OF INVENTION: USING
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDREAT. BORUCKI
STREET: 9330 ZIONSVILLE ROAD
CURRENT APPLICATION DATA:
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CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/378,761A
FILING DATE: 26-JAN-1995
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LENGTH: 290 amino acids
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                                                                                                                                                                 STREET: 9330 ZIONSV
CITY: INDIANAPOLIS
                                                                                                                                   COUNTRY:
                                                                                                                                                           STATE:
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STRANDEDNESS: single
TOPOLOGY: linear
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OPERATING SYSTEM: PC-DOS/MS-DOS
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94.98;
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; TOPOLOGY: 1:
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                                                                                                                                                                                                                                                                                                        SEQ ID NO:4:
                                                                                                                                                                                                        Matches 188;
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 26-JAN-1995
ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: US 0
FILING DATE: 26-JAN-1995
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                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 49
                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: DNA ENCODING INACTIVE PRECURSOR AND
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: WALSH, TERENCE A.; HEY, TIMOTHY D.; MORGAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
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REGISTRATION NUMBER: 33
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                                                                                                                                                                                                                                                                                                                      FILING DATE: 11-JUN-1990
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                                                                                                                                                                                                                                                                                        LENGTH: 290
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                                                                                                                                                                                                                        ocal Similarity
171 FQYIEGEMRTRIRYNRRS 188
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                                                                                                                                      25 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
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                                                                                                                                                                                                                   Score 951; DB 6;
Pred. No. 2e-102;
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                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                        Indels 10;
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US-08-356-786-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Oppermann, Hermann APPLICANT: Houston, L. L. APPLICANT: Ring, David B. TITLE OF INVENTION: Biosynthet TITLE OF INVENTION: Marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edmund R. Pitcher, Testa, Hurwitz, & Thibeault
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: CR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 07/8
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Ditcher Edmind B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                     98.4%;
Local Similarity 94.9%;
ses 188; Conservation
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                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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184
                                                                       124 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR
                                                                                          111 GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 170
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                                    171 FQYIEGEMRTRIRYNRRS 188
                                                                                                                                                64 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                                                                                                                 51 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG 110
                                                                                                                                                                                                                                         1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILV
                                                                                                                                                                                                                       4 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLTTGADVRHEIPVLPNRVGLPINQRFILV
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FOYIEGEMRTRIRYNRRS 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Massachusetts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Exchange Place, 53 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                         534 amino acids
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SYSTEM: PC-DOS/MS-DOS
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Pred. No. 4.9e-102;
Prediches 0;
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Search completed: September 16, 2003, 11:51:47

183

Job time : 11.7099 secs

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Result
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
: /cgn2_6/ptodata/2/pubpaa/USO9A_PUBCOMB.pep:*
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2 US-10-127-890-4
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             US-10-127-890-107
US-10-127-890-106
US-10-127-890-110
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Sequence 39, Appl
Sequence 4, Appli
Sequence 34, Appli
Sequence 34, Appli
Sequence 3, Appli
Sequence 7, Appli
Sequence 4, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 107, App
Sequence 107, App
Sequence 110, App
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Sequence 1, Appli
Sequence 39, Appl
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92-793A-7 27-890-3 27-890-12 27-890-12	09-792-793A-7 -09-792-793A-8 -10-127-890-10 -09-792-793A-3 -09-792-793A-7	20440W	-10-127-890- -10-127-890- -10-127-890- -10-127-890- 09-765-527-2 09-765-527-2 -10-127-890-	US-10-127-890-111 US-09-765-527-247 US-10-127-890-2 US-10-127-890-99 US-10-127-890-100 US-10-127-890-101 US-10-127-890-101 US-10-127-890-102 US-10-127-890-103
Sequence 76, Appl Sequence 3, Appli Sequence 127, App Sequence 128, App	795	9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	10 10 259 253 251	Sequence 111, App Sequence 247, App Sequence 2, Appli Sequence 9, Appl Sequence 100, App Sequence 101, App Sequence 102, App Sequence 103, App

## ALIGNMENTS

RESULT 1 US-10-127-890-1

Sequence 1, Application US/10127890 Publication No. US20030166196A1 GENERAL INFORMATION:

```
APPLICANT: Better, Marc D.
Carroll, Stephen F.
Studnika, Gary M.

TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
NUMBER OF SEQUENCES: 173

CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60661
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATIOS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, version #1.25
CURRENT APPLICATION NUMBER: US/08/46,360
FILING DATE: 23-Apr-2002
CLASSIFICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1994
APPLICATION NUMBER: US/08/646,360
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US/08/646,360
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US/08/64,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 19-DUN-1992
FILING DATE: 19-JUN-1992
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В
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                                                                                                                                                                                            SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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Matches
                  Best Local Similarity
                                  Query Match
                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 09/538,873
PRIOR FILING DATE: 2000-03-30
PRIOR APPLICATION NUMBER: 60/126,826
PRIOR FILING DATE: 1999-03-30
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                               APPLICANT: BALJUNA, ROXANA G.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS OF
TITLE OF INVENTION: PROTEINACEOUS COMPOUNDS
FILE REFERENCE: UTSD:884US
CURRENT APPLICATION NUMBER: US/10/282,935
CURRENT FILING DATE: 2002-10-29
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: VITETTA, ELLEN S.
APPLICANT: GHETIE, VICTOR F.
APPLICANT: SMALLSHAW, JOAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                    OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: Peptide
                                                                                                                        FEATURE:
                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                         TYPE: PRT
                                                                                                                                                                        LENGTH: 267
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NAME: MCNICholas, Janet M.
REGISTRATION NUMBER: 32,918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181
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 186;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 07/787,567 FILING DATE: 04-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 267 amino acids
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94.9%;
                97.4%;
94.9%;
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              Score 941; DB 12;
Pred. No. 8.8e-100;
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Pred. No. 6.2e-101;
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 Mismatches
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                               Length 267;
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                                                                                                      Synthetic
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; LENGTH: 247
TYPE: PRT
; ORGANISM: Trichosanthews kirilowii
US-09-792-793A-39
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
FILE REFERENCE: 25020-601D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/792,793A
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 93
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                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Better, Marc D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          116 TAAGKIRENIPLGLPALDSAITTLFYYNAN----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 YDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQ 172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59 SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 117 :::::|:||| | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
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Similarity 38.9%;
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STREET: 500 West Madison Street, CITY: Chicago
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                                                                                                                                                                                                                               Proteins
                                                                                                                                                                                                                                                                                                                            Gary M.
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Pred. No. 2.6e-30;
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                                                                                                            Sequence 4, Application US/10280679B Publication No. US20030150019A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
APPLICANT: Large Scale Biology Corporation
TITLE OF INVENTION: Monopartite RNA Virus Transformation Vectors
FILE REFERENCE: LSBC-01109-US03
CURRENT APPLICATION NUMBER: US/10/280,679B
CURRENT FILING DATE: 2000-10-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                         171 IGKRV 175
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                                                                                                                                                                                                                                                                                                                     178 MRTRI 182
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FILING DATE: 12-MAX-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
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FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                          US-09-792-793A-34
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US-09-792-793A-34
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; SEQ ID NO 4
FURTH: 289
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 34, Application US/09792793A Patent No. US20020168370A1 GENERAL INFORMATION:
                                                                                                                                                                       SOFTWARE: PatentIn Ver. SEQ ID NO 34
      Best Local Similarity Matches 65; Conserv
                                              Query Match
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Best Local S
                                                                                                                                                                                                                                                                             APPLICANT: McDonald, John R.
APPLICANT: Coggins, Philip
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING SECONDARY TISSUE DAMAGE
TITLE OF INVENTION: OTHER INFLAMMATORY CONDITIONS AND DISORDERS
FILE REFERENCE: 25020-601D
                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/792,793A CURRENT FILING DATE: 2001-02-22 NUMBER OF SEQ ID NOS: 93
                                                                                                         LENGTH: 247
TYPE: PRT
ORGANISM: Bryonia dioica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1988-02-26
PRIOR APPLICATION NUMBER: 07/160,771
PRIOR FILING DATE: 1988-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 07/310,881 PRIOR FILING DATE: 1989-02-17 PRIOR APPLICATION NUMBER: 07/160,766
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TYPE: PRT
ORGANISM: Chinese cucumber protein alpha-trichosanthin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 08/484,341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 09/557,941 PRIOR FILING DATE: 2000-04-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 07/739,143 FILING DATE: 1991-08-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1991-01-16
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APPLICATION NUMBER: 07/641,617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139 TAAGKIRENIPLGLPALDSAITTLFYYNAN-----SAASALMVLIQSTSEAARYKFIEQQ 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 SYTLALDYTNAYVYGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 VSFRLSGATSSSYGVFISNLR---KALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADE 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 INFTTAGATVQSYTNFIRAVRGRLTVLPN------RVGLPINQRFILVELSNHAEL 58
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      Conservative
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31.6%; Score 305; DB 10; 35.7%; Pred. No. 9.7e-27; tive 45; Mismatches 56;
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                                            Length 247;
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US-10-282-935-3
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                                                              Sequence 7, Application US/10127890 Publication No. US20030166196A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3, Application US/10282935 Publication No. US20030143193A1 GENERAL INFORMATION:
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TYPE: PRT
ORGANISM: Abrus |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: BALUNA, ROXANA G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODIFYING TOXIC EFFECTS

TITLE OF INVENTION: PROTEINACEOUS COMPOUNDS

FILE REFERENCE: UTSD:884US

CURRENT APPLICATION NUMBER: US/10/282,935

CURRENT FILING DATE: 2002-10-29

PRIOR APPLICATION NUMBER: 09/538,873

PRIOR FILING DATE: 2000-03-30

PRIOR APPLICATION NUMBER: 60/126,826

PRIOR APPLICATION NUMBER: 60/126,826

PRIOR APPLICATION DATE: 1999-03-30

NUMBER: 05 SE0 ID NOS: 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.1
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                                          APPLICANT: Better, Marc D.
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                                                                                                                                                                                                                176
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                                                                                                                                                                                                                                                                                              119 WAHQSRQQIPLGLQALTHGIS---FFRSGGNDNEEKARTLIVIIQMVAAAARFRYISNRV 175
                                                                                                                                                                                                                                                                                                                                        119 LAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEM 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 VAVDVTNVYIMGYLAGDVSYFF---NEASATEAAKFVFKDAKKKVTLPYSGNYERLQTAA 118
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                                                                                                                                                                                                                                                                                                                                                                                    EVGIDVTNAYVVAYRAGTQSYFLRDAPSSASD-----YLFTGT-DQHSLPFYGTYGDLER 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IKFSTEGATSQSYKQFTEALRERLRGGLIHDIPVLPDPTTLQERNRYITVELSNSDTESI 64
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Carroll, Stephen F. Studnika, Gary M.
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US-10-127-890-4

Sequence 4, Application US/10127890

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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: MCNicholas, Janet M.
REGISTRATION NUMBER: 32,918
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                       119 GKPREKIPIGLPALDSAISTLLHYDS----TAAAGALLVLIQTTAEAARFKYIEQQIQE 173
                                                                                                                                                                                                 121 GNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRT 180
                                                                  174 R 174
                                                                                                              181 R 181
                                                                                                                                                                                                                                                62 VAVDVTNVYIMGYLADTTSYFF---NEPAAELASQYVFRDARRKITLPYSGNYERLQIAA 118
                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/646,360
FILLING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILLING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILLING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILLING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
                                                                                                                                                                                                                                                                                                                                     2 VSFRLSGADPRSYGMFIKDLRNALPFREKVYNIPLLLPSVSGAGRYLLMHLFNYDGKTIT 61
                                                                                                                                                                                                                                                                                                                                                                                  9 INFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPI-----NQRFILVELSNHAELSVT 61
                                                                                                                                                                                                                                                                                                                                                                                                                               63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 263 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                    28.3%; Score 273; DB 12; 34.8%; Pred. No. 5e-23;
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INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 60661
COMPUTER READABLE FORM:
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FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
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173 VATN 176
                                     182 IRYN 185
                                                                        118 KIRENIDLGLPALSSAITTLFYYNA-----QSAPSALLVLIQTTAEAARFKYIERHVAKY 172
                                                                                               62 VAIDVTNVYVVAYRTRDVSYFF----KESPPEAYNILFKGTR-KITLPYTGNYENLQTAAH 117
                                                                                                                                                                                         62 LALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAG 121
                                                                                                                                                                                                                                                              9 INFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPI------NQRFILVELSNHAELSVT 61
                                                                                                                                                                                                                                                                                                                        63;
                                                                                                                                                                                                                                   VNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISDSRRFILLDLTSYAYETIS 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: PCT/US94/05348 FILING DATE: 12-MAY-1994 APPLICATION NUMBER: US 08/064,691 FILING DATE: 12-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 312/707-8889
TELEFAX: 312/707-9155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: McNicholas, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 07/787,567 FILING DATE: 04-NOV-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 263 amino acids
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                                                                                                                                                                                                                                                                                                                    39;
                                                                                                                                                                                                                                                                                                                                       Score 272; DB 12;
Pred. No. 6.6e-23;
                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                    66;
                                                                                                                                                                                                                                                                                                                                                     Length 263;
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Best Local Similarity
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APPLICANT: Better, Marc D.
                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                      118 QLAGNLRENIELGNGPLEEATSALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 177
                                                                      58
                                                                                                         58 LSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLE 117
                                                                                                                                                                                                                                             58;
                                                                                                                                                                                               9 INFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPIN------QRFILVELSNHAE 57
                                                               KAITVAVDVSQLYIMGYLVNSTSYFF---NESDAKLASQYVFKGSTIVTLPYSGNYEKLQ 114
                                                                                                                                                    VRFSLSGSSSTSYSKFIGDLR----KALPSN-GTVYNLTILLSSASGASRYTLMTLSNYDG 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 09-DEC-1992
APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
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TELEX: 650 388-1248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/787,567 FILING DATE: 04-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/646,360 FILING DATE: 13-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 248 amino acids
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STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                           Conservative
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46; Mismatches
                                                                                                                                                                                                                                                             Score 257.5; DB 12; Pred. No. 2.8e-21;
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  Indels
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US-09-347-064-8
; Sequence 8, Application US/09347064A
; Patent No. US20020045208A1
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CURRENT APPLICATION NUMBER: US/09/347,064A
CURRENT FILING DATE: 1999-07-02
EARLIER APPLICATION NUMBER: PCT/EP98/0009
EARLIER APPLICATION NUMBER: PCT/EP98/0009
EARLIER FILING DATE: 1998-01-02
EARLIER FILING DATE: 1998-01-02
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EARLIER FILING DATE: 1998-01-02
EARLIER FILING DATE: 1998-01-02
EARLIER FILING DATE: 1998-01-02
                                                                                                              TITLE OF INVENTION: Recombinant Fusion Proteins Based on TITLE OF INVENTION: Ribosome-Inactivating Proteins of the mistletoe Viscum TITLE OF INVENTION: album FILE REFERENCE: 09282-5 CURRENT APPLICATION NUMBER: US/09/347,064A CURRENT FILING DATE: 1999-07-02
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APPLICANT: Schmidt, Arno
APPLICANT: Zinke, Holger
                   EARLIER APPLICATION NUMBER: PCT/EP98/00009
EARLIER FILING DATE: 1998-01-02
EARLIER APPLICATION NUMBER: EP 97 10 0012.0
EARLIER FILING DATE: 1997-01-02
                                                                                                                                                                                                                                                           APPLICANT: Eck, Jurgen
APPLICANT: Schmidt, Arno
APPLICANT: Zinke, Holger
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NUMBER OF SEQ ID NOS: 38
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ORGANISM: Viscum album
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     182 NSGASFLPDVYMLELETSWGQQSTQVQHS 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 -RDQIPLGIDQLIQSVTALRF----PGGSTRTQARSILILIQMISEAARFNPILWRARQYI 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 ALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGN 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 AIDVTNLYVVAYQAGDQSYFLR-DAPRGAE--THLFTGT-TRSSLPFNGSYPDLERYAGH 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARF------QYI 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THQTTGEEYFRFITLLRDYVSSGSFSNEIPLLRQSTIPVSDAQRFVLVELTNQGGDSITA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26.3%;
35.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 254; DB 9; Length 252; Pred. No. 7.2e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DЬ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 107, Application US/10127890 Publication No. US20030166196A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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ORGANISM: Viscum album
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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                                                                                                  FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 04-NOV-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Studnika, Gary M.
TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
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Carroll, Stephen F.
    REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 ALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAGN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AIDVTNLYVVAYQAGDQSYFLR-DAPRGAE--THLFTGT-TRSSLPFNGSYPDLERYAGH 124
                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US94/05348 FILING DATE: 12-MAY-1994 APPLICATION NUMBER: US 08/064,691 FILING DATE: 12-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 23-Apr-2002 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                APPLICATION NUMBER: US 07/988,430 FILING DATE: 09-DEC-1992 APPLICATION NUMBER: US 07/901,707
                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/646,360 FILING DATE: 13-MAY-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/10/127,890
                                                      REGISTRATION NUMBER:
                                                                              NAME: McNicholas, Janet M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26.3%; Score 254; DB 9; Length 252; 35.9%; Pred. No. 7.2e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -GEMRTRIRYN 185
                                                      32,918
                                200-70.P4
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RESULT 14
US-10-127-890-106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 107: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                      ZIP: 60661
COMPUTER READABLE FORM:
TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: McAndrews, Held & Malloy, Ltd.
STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 107:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Better, Marc D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175 NQIRNNFQQRIR 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 QLAGN--LRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 EIAIDVTSVYVVGYQVRNRSYFFKDAPD-----AAYEGLFKNTIKTR--LHFGGSYPSLE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TLALDVTNAYVVGYRAGNSAYFFH--PDNQEDAEAITHLFTD-VQNRYTFAFGGNYDRLE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9 INFTTAGATYQSYTNFIRAVRGRLTYLPNRVGLPINQR-----FILVELSNHAELSV 60
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                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
             APPLICATION NUMBER: US 07/787,567
                                APPLICATION NUMBER: US 07/901,707 FILING DATE: 19-JUN-1992
                                                                   APPLICATION NUMBER: US 08/064,691
FILING DATE: 12-MAY-1993
APPLICATION NUMBER: US 07/988,430
FILING DATE: 09-DEC-1992
                                                                                                                                          APPLICATION NUMBER: PCT/US94/05348 FILING DATE: 12-MAY-1994
                                                                                                                                                                              APPLICATION NUMBER: US/08/646,360 FILING DATE: 13-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: Illinois
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FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
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TELEFAX: 312/707-9155
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Pred. No. 6.8e-20;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 17: CORRESPONDENCE ADDRESS:
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NAME: MCNicholas, Janet M.
REGISTRATION NUMBER: 32,918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             175 NQIRNNFQQRIR 186
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                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                           CITY: Chicago
         FILING DATE:
                                                                                                                                                                                                                                                                                                                                            STATE: Illinois
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; MOLECULE TYPE: protein ; SEQUENCE DESCRIPTION: SEQ ID NO: 106: US-10-127-890-106
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TELEX: 650 388-1248
INFORMATION FOR SEQ ID NO: 106:
SEQUENCE CHARACTERISTICS:
                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/646,360
FILING DATE: 13-MAY-1996
APPLICATION NUMBER: PCT/US94/05348
FILING DATE: 12-MAY-1994
                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/127,890
FILING DATE: 23-Apr-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Better, Marc D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Immunotoxins Comprising Ribosome-Inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 ---GEKAYRETTDLGIEPLRIGIKKLDENAIDNYKPTEIASSLLVVIQMVSEAARETFIE 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 QLAGN--LRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 EIAIDVTSVYVVGYQVRNRSYFFKDAPD-----AAYEGLFKNTIKTR--LHFGGSYPSLE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 TLALDVTNAYVVGYRAGNSAYFFH--PDNQEDAEAITHLFTD-VQNRYTFAFGGNYDRLE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 VSFSTCGATYITYVNFLNELRVKLKPEGNSHGIPLLRKKCDDPGKCFVLVALSNDNGQLA 64
                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION NUMBER: US 08/064,691 FILING DATE: 12-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: McAndrews, Held & Malloy, Ltd. STREET: 500 West Madison Street, 34th floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 312/707-8889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/10127890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carroll, Stephen F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gary M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 244.5; DB 1
Pred. No. 8.9e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200-70.P4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64; . Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             251;
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; TOPOLOGY: linear;; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 110: US-10-127-890-110
                                  Qy
                                                                                   Б
                                                                                                                    Qy
                                                                                                                                                                  Ф
                                                                                                                                                                                                          Qy
                                                                                                                                                                                                                                                 Db
                                                                                                                                                                                                                                                                                                Qy
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APPLICATION NUMBER: US 07/901,707
FILING DATE: 19-JUN-1992
APPLICATION NUMBER: US 07/787,567
FILING DATE: 19-WOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MCNICHOLAS, Janet M.
REGISTRATION NUMBER: 32,918
REFERENCE/DOCKET NUMBER: 200-70.P4
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECAX: 312/707-8889
TELEX: 650 388-1248
INFORMATION FOR SEQUENCE CHARACTERISTICS:
LENGTH: 251 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                   Query Match 25.3%; Score 244.5; DB 12; Length 251; Best Local Similarity 36.5%; Pred. No. 8.9e-20; Matches 70; Conservative 30; Mismatches 65; Indels 27; Gaps
                                                                                 118 QLAGN--LRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAREQYIE 175
175 NOIRNNFOORIR 186
                                            176 GEMRT----RIR 183
                                                                                                                                                                         65 EIAIDVTSVYVVGYQVRNRSYTFKDAPD-----AAYEGLFKNTIKTR--LHFGGSYPSLE 117
                                                                                                                                                                                                                 61 TLALDVINAYVYGYRAGNSAYFFH--PDNQEDAEAITHLFTD-VQNRYTFAFGGNYDRLE 117
                                                                                                                                                                                                                                                             5 VSFSTCGATVITYVNFLNELRVKLKPEGNSHGIPLLRKKADDPGKAFVLVALSNDNGQLA 64
                                                                                                                                                                                                                                                                                       9 INFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPI------NQRFILVELSNHAELSV 60 ::|:| | | | : | : | : | : | | | | |
                                                                                                                                                                                                                                                                                                                                                        8;
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Search completed: September 16, 2003, 12:09:56 Job time: 19.4426 secs

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GenCore version 5.1.6

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 16, 2003, 11:40:32; Search time 12.1928 Seconds (without alignments) 1482.817 Million cell updates/sec

Title: US-10-083-336A-4

Perfect score: 966
Sequence: 1 IFPKQYPIINFTTAGATYQS......ARFQYIEGEMRTRIRYNRRS 188

Scoring table: BLOSUM62 Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Database :

PIR\_76:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

#### SUMMARIES

	Score	ch	Length [	DB	ID	Description
1	51		576	r i	RLCSD	ricin D precursor
2	861.5	89.2	564	بر	RLCSAG	precu
ω	w		289	_	RLTZT	rRNA N-glycosidase
4			528	2	S32431	cursor
5	27		562	2	S16022	
6	326		247	N	JU0393	in'
7	326		247	N	JC5032	karasurin-B - Tric
8	326		289	N	JC5606	S
؈	323	•	527	N	S32430	recur
10			251	N	C39761	0
11	303.5	31.4	528	_	TZLSA	å.
12	•	•	2/8	\ N	\$23519	beta-luffin - smoo
٠ <u>٢</u>		•	250	κ.	JNOIOS	luffin-b - smooth
14	1 .		277	۸,	\$22494	rRNA N-glycosidase
	2/3		982	-	RLPUGG	rRNA N-glycosidase
16	273		570	N	S62627	agglutinin I precu
. 1.7	272	28.2	286	Ν	\$25560	A N-glycos
. L	270		245	2	JC4840	rRNA N-glycosidase
19	265		286	N	JC4235	N-glycosidas
20	264		254	2	PD0018	letoe lectin
21	243.5		316	N	JT0753	N-qlycosidas
22	~		294	N	S28421	N-qlycosidas
23	174		278	N	A39817	N-qlycosidas
24	170		313	2	S17757	N-qlycosidas
25	168.5		261	N	JE0401	viral protein
26	148.5		289	Ν	T12573	A N-qlv
27	138		272	N	JC4811	vulgin - beet
28	131		253	N	S28542	rRNA N-glycosidase
29	127	13.1	253	2	S28539	N-glycosidas

11.2 319 2 11.1 318 2	108 11.2	108 11.2 319 2	109 11.3 319 2	110 11.4 236 2	112 11.6 280 2	114 11.8 280 1	115 11.9 253 2	116 12.0 275 2	116.5 12.1 293 2	121 12.5 310 2	121 12.5 292 1	123 12.7 253 2	124 12.8 283 2	127 13.1 253 2	
Shiga toxin 2 subu Shiga-like toxin I	Shiga toxin 2 subu	shiga-like toxin I	hypothetical prote	rRNA N-glycosidase	protein synthesis	rRNA N-qlycosidase	rRNA N-glycosidase	tritin - wheat	rRNA N-glycosidase	ribosome-inactivat	rRNA N-glycosidase	rRNA N-glycosidase	rRNA N-glycosidase	rRNA N-glycosidase	

## ALIGNMENTS

A; Molecule type: protein A; Residues: 315-383, 'PS', 386-576 <ara> R; Funatsu, G; Kimura, M; Funatsu, M. Agric. Biol. Chem. 43, 2221-2224, 1979 A; Title: Primary structure of Ala chain of ricin D. A; Reference number: A03374 A; Accession: A03374 A; Molecule type: protein</ara>	K;AIAKI, T.; FUNAISU, G. FEBS Lett. 191, 121-124, 1985 A;Title: Revised amino acid sequence of the B-chain of ricin D due to loss of tryptop A;Reference number: A24010 A;Accession: A24010	A;Accession: A03372 A;Molecule type: protein A;Molecules: 36-97,'Q',99-109,'S',111-269,'D',272-283,'L',285-288,290-302 <yos> A;Note: This paper cites the others in the series providing experimental details for</yos>	A; Cross Telefences: GB:X01388; NID:g21077; PIDN:CAA26230.1; PID:g21078 R; Yoshitake, S.; Funatsu, G.; Funatsu, M. Agric. Biol. Chem. 42, 1267-1274, 1978 A; Title: Isolation and sequences of peptic peptides, and the complete sequence of Ile A; Reference number: A03372	A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-576 <tre> A; Cross-references: EMBL: x52908; NID: g21084; PIDN: CAA37095.1; PID: g21085 R; Lamb, F.I.; Roberts, L.M.; Lord, J.M. Eur. J. Biochem. 148, 265-270, 1985</tre>	A;Cross-references: GB:X03179; NID:g21082; PIDN:CAA26939.1; PID:g21083 R;Tregear, J.W.; Roberts, L.M. Plant Mol. Biol. 18, 515-525, 1992 A;Title: The lectin gene family of Ricinus communis: cloning of a functional ricin ge A;Reference number: S20513; MUID:92163016; PMID:1371405 A;Accession: S20513	A;Title: Genomic cloning and characterization of a rigin gene from Riginus communis. A;Reference number: A24041; MUID:86067214; PMID:2999712 A;Accession: A24041 A;Accession: Accession: Acces	RESULT 1  RICSD  RICSD  RICH  RICH

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Ryntenber, E.; Robertus, J.D.

Rynteins 10, 260-269, 1991

RyTitle: Structure of ricin B-chain at 2.5 angstrom resolution.

A; Fitle: Structure of ricin B-chain at 2.5 angstroms

A; Fitle: Structure of ricin B-chain at 2.5 angstroms

A; Fitle: Structure of ricin A-chain at 2.5 angstroms

A; Contents: annotation; X-ray crystallography, 2.5 angstroms

A; Fitle: Structure of ricin A-chain at 2.5 angstroms

A; Fitle: Structure of ricin A-chain at 2.5 angstroms

A; Fitle: Structure of ricin A-chain at 2.5 angstroms

A; Fitle: Structure of ricin A-chain at 2.5 angstroms

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A; Fitle: Structure of ricin A-chain at 2.5 angstroms

A; Fitle: Structure of ricin A-chain at 2.5 angstroms

C; Comment: The functional molecule is a disulfide-linked dimer of A and B chains, which C; Comment: The function is cytotoxic and very polsonous to animals.

C; Superfamily: ricin: Structure at 2.5 angstroms

C; Superfamily: ricin: RNA N-glycosidase homology

C; Keywords: duplication; glycosidase homology

C; Keywords: duplication; glycosidase; homology

C; Superfamily: ricin: RNA N-glycosidase; homology

A; S
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A;Note: this paper, one of a series, summarizes the experimental details for the determing:R;Ready, M.P.; Kim, Y.; Robertus, J.D.
Proteins 10, 270-278, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Rutenber, E.; Robertus,
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                                                                                          R;Roberts, L.M.; Lamb, I.F.; Papp
J. Biol. Chem. 260, 15682-15686,
A;Title: The primary sequence of
A;Reference number: A24261; MUID:
A;Accession: A24261
                                                                                                                                                                                                                                                               C;Species: Ricinus communis (castor bean)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 16-Jul-1999
C;Accession: A24261; A24210
                                                                                                                                                                                                                                                                                                                                                         agglutinin precursor - castor bean N; Contains: rRNA N-glycosidase (EC 3.2.2.22)
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A; Residues: 1-564 <F
A; Cross-references:
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                                                               A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAAR 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GNYDRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFITCIQMISEAAR
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      GB:M12089; NID:g169700; PIDN:AAA33869.1; PID:g169701
                                                                                                                                                                                                                             I.F.; Pappin, D.J.C.; Lord, J.M.
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                                                                                                                                      MUID:86059449;
                                                                                                                                                                 Ricinus communis agglutinin. Comparison with ricin.
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                                                                                                                                         PMID: 2999130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              171
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F.25-290/Product: agglutinin chain A #status predicted <ACH>
F.35-281/Domain: rRNA N-glycosidase homology <RNC>
F.30-564/Product: agglutinin chain B #status experimental <BCH>
F.303-564/Product: agglutinin chain B #status experimental <ACH>
F.303-564/Product: agglutinin chain B #status experimental <ACH>
F.319-361,362-402,405-443,450-485,489-528,531-564/Region: 40-residue repeats
F.319-361,362-3402,405-481,450-486,489-528,531-564/Region: 40-residue repeats
F.319-361,322-3104,322/Binding site: substrate (Tyr. Tyr. Glu, Asn) #status predicted
F.200,203/Active site: Glu, Arg #status predicted
F.200,203/Active site: Glu, Arg #status predicted
F.282-306,322-341,365-382,453-466,492-509/Disulfide bonds: #status predicted
F.324,337,348/Binding site: N-acetylgalactosamine (Asp, Gln, Asn) #status predicted
F.324,337,348/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
F.356,557/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Keywords: duplication; glycoprotein; glycosidase; hydrolase; F;1-24/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein A;Residues: 303-325,'F',327-330,'T',332-361,'D',363-373,'G',375-403,'T',405-551,'V',5 C;Comment: This protein has strong agglutinating activity and weak cytotoxicity compa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A24210
A; Accession: A24210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Araki, T.; Yoshioka, Y.; Funatsu, G.
Biochim. Biophys. Acta 872, 277-285, 1986
A;Title: The complete amino acid sequence of the B-chain of the Ricinus communis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Superfamily: ricin; rRNA N-glycosidase homology
                                                                                                                                                                                                                                                                                                                                                           51 ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 IFPKQYPIINFTTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                 IFPKQYPIINFTTADATVESYTNFIRAVRSHLTTGADVRHEIPVLPNRVGLPISQRFILV
FOYIEGEMETRIRYNERS
                                                                 FOYIEGEMRTRIRYNRRS 188
                                                                                                                                          GNYDRLEQL-GGLRENIELGTGPLEDAISALYYYSTCGTQIPTLARSFMVCIQMISEAAR 203
                                                                                                                                                                                                                                                                                     ELSNHAELSVTLALDVTNAYVVGCRAGNSAYFFHPDNQEDAEAITHLFTDVQNSFTFAFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89.2%;
   221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 861.5; DB 1 Pred. No. 3.9e-71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
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                                                                                                                                                                                                                               170
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rRNA N-glycosidase (EC 3.2.2.22) alpha-trichosanthin precursor [validated] - Mongolia N;Alternate names: alpha-TCS; type I ribosome-inactivating protein C;Species: Trichosanthes kirilowii (Mongolian snake-gourd)
C;Becies: Trichosanthes kirilowii (Mongolian snake-gourd)
C;Date: 30-Sep-j988 #sequence\_revision 26-Jan-1996 #text\_change 23-Mar-2001
C;Accession: JT0566; A36274; JC1093; A36273; JT0003
C;Accession: JT0566; A36274; JC1093; A36273; JT0003
R;Shaw, P.C.; Yung, M.H.; Zhu, R.H.; Ho, W.K.K.; Ng, T.B.; Yeung, H.W.
Gene 97, 267-272, 1991
A;Title: Cloning of trichosanthin cDNA and its expression in Escherichia coli.
A;Reference number: JT0566; MUID:91153657; PMID:1999291
A;Accession: JT0566
A;Molecule type: mRNA
A;Recsidues: 1-289 <SHA>
A;Cross-references: GB:M3458; NID:g170536; PIDN:AAA34207.1; PID:g170537
A;Experimental source: tuber
R;Chow, T.P.; Feldman, R.A.; Lovett, M.; Piatak, M.
J. Biol. Chem. 265, 8670-8674, 1990
A;Title: Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a type I
A;Reference number: A36274; MUID:90256790; PMID:2341400
A;Residues: 1-233, 'T', 235-246, 'M', 248-289 <CHO>
A;Cross-references: GB:J05434; NID:g170534; PIDN:AAA34206.1; PID:g170535
A;Accession: J05033; MUID:g170534; PIDN:AAA34206.1; PID:g170535
A;Accession: J05033; MUID:g170534; PIDN:AAA34206.1; PID:g170535

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RESULT 4
S32431
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C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
C;Function:
A;Punction:

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A;Reference number: A66711; PDB:ITCS
A;Contents: annotation; X-ray crystallography, 1.7 angstroms, with NADPH, residues 24-R;Xiong, J.P.; Xia, Z.X.; Wang, Y. Nat. Struct. Biol. 1, 695-700, 1994
A;Title: Crystal structure of trichosanthin-NADPH complex at 1.7 Angstroms A;Reference number: A5862; MUID:95360714; PMID:7634073
A;Contents: annotation; X-ray crystallography, 1.7 angstroms
A;Contents: annotation; X-ray crystallography, 1.7 angstroms
A;Contents: annotation; X-ray crystallography, 1.7 angstroms
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A;Title: Scientific evaluation of Tian Hua Fen (THF): history, chemistry and application A;Reference number: JT0003
A;Accession: JT0003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Experimental source: tuber R; Huang, Q.; Liu, S.; Wang, Y.; Jin, S.; Wang, submitted to the Brookhaven Protein Data Bank, A; Reference number: A67091; PDB: LMRJ
N; Contains: rRNA N-glycosidase
                                            abrin-d precursor -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F; 24-270/Product: F; 27-266/Domain: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-72, 'V', 74-90, 'S', 92-233, 'T', 235-267, 'D', 269-289 <ZHE>
A; Cross-references: GB:S70176; NID:9547148; PIDN:AAB31048.1; PID:9547149
A; Croslins, E.J.; Robertus, J.D.; Lopresti, M.; Stone, K.L.; Williams, K.R.; Wu,
J.Biol. Chem. 265, 8665-8669, 1990
J.Biol. Chem. 265, 8665-8669, 1990
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A; Residues: 24-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues:
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271-289/Domain: carboxyl-terminal propeptide #status predicted <CTP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    118 QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE
                                                                                                                                                                                                                                                                               194 IGKRV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82 TISVAIDVTNVYIMGYRAGDTSYFF---NEASATEAAKYVFKDAMRKVTLPYSGNYERLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25 VSFRLSGATSSSYGVFISNLR----KALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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24-56,'L',58-59,'I',61-71,'I',73-81,85-86,'L',88-92,'DAGLPRNAVL',93-142,'GL
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                                                                                                                                                                                                                                                                                                                                                                                 MRTRI 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAAGKIRENIPLGLPALDSAITTLFYYNAN----SAASALMVLIQSTSEAARYKFIEQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFTTAGATVQSYTNFIRAVRGRLTVLPN-----RVGLPINQRFILVELSNHAEL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
Indian licorice (fragment) qlycosidase (EC 3.2.2.22)
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F;7-246/Domain: rRNA N-glycosidase homology <RNG>
F;261-528/Product: abrin-d chain B #status predicted <BCH>
F;283-325,326-366,369-407,414-449,453-495-528/Region: 40-residue repeats
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted
F;74,113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #status predicted
F;164,167/Active site: Glu, Arg #status predicted
F;164,167/Active site: Glu, Arg #status predicted
F;200,253,361,401,402/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;288,312/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
F;288,312/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
F;500,521/Binding site: N-acetylgalactosamine (Asp, Asn) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Comment: Abrin consists of an A chain, which inhibits protein synthesis by inactiva The A and B chains are linked by a single disulfide bond, which is essential for tox C;Superfamily: ricin; rRNA N-glycosidase homology C;Keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin F;1-25//Product: abrin-d chain A *status predicted <ACH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R:Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
J. Mol. Biol. 229, 263-267, 1993
A;Title: Primary structure of three distinct isoabrins determined by cDNA sequencing.
A;Reference number: S32429; MUID:93132798; PMID:8421313
A;Accession: S32431
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C;Date: 30-Sep-1993 #sequence_revision 01-Aug-1997 #text_change 01-Aug-1997
C;Accession: S32431; S34408
N;Contains: rRNA N-glycosidase (EC 3.2.2.2)
C;Species: Abrus precatorius (Indian licorice)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-
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A;Residues: 1-169,'C',171-320,'L',322-528 <HU2>
A;Cross-references: GB:M98346
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R;Hung, C.; Lee, M.; Lee, T.; Lin, J.
submitted to the EMBL Data Library, March 1993
                                                                                                 abrin-c precursor - Indian licorice
                                                                                                                                   S16022
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A; Accession: S34408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         EQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIOMISEAARFQYIEG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESIEVGIDVTNAYVVAYRAGSQSYFL---RDAPASASTYLFPGTQ-RYSLRFDGSYGDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QDQVIKFTTEGATSQSYKQFIEALRQRLTGGLIHDIPVLPDPTTVEERNRYITVELSNSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QYPIINFTTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVELSNHA 56
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43.9%;
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Pred. No. 3.5e-22
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A;Cross-references: EMBL:X55667; NID:g16084; PIDN:CAA39202.1; PID:g16085 C;Comment: Abrin consists of an A chain, which inhibits protein synthesis by inactiva The A and B chains are linked by a single disulfide bond, which is essential for tox

A; Molecule type: DNA A; Residues: 1-562 < WOO>

A;Status: preliminary

A; Reference number: A; Accession: S16022

C; Accession: S16022

19-Mar-1997 #text\_change 20-Aug-1999

R:Wood, K.A.; Lord, J.M.; Wawrzynczak, E.J.; Piatak, M. Eur. J. Biochem. 198, 723-732, 1991
A;Title: Preproabrin: genomic cloning, characterisation A;Reference number: S16022; MUID:91266957; PMID:2050149

and the

expression of the A-c

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C;Superfamily: ricin; rRNA N-glycosidase homology
C;Reywords: duplication; glycoprotein; glycosidase; hydrolase; lectin; pyroglutamic
F;35-285/Product: abrin-c chain A *status predicted <ACH>
F;41-280/Domain: rRNA N-glycosidase homology <RNG>
F;295-562/Product: abrin-c chain B *status predicted <BCH>
F;317-359,360-400,403-441,448-4483,487-526,529-562/Region: 40-residue repeats
F;317-359,360-400,403-441,448-4483,487-1516-362/Region: 40-residue repeats
F;318-Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) *status predicted
F;108,147,229,230/Binding site: substrate (Tyr, Tyr, Glu, Asn) *status predicted
F;198,201/Active site: Glu, Arg *status predicted
F;3198,301,339,435,436/Binding site: carbohydrate (Asn) (covalent) *status predicted
F;322,346/Binding site: N-acetylgalactosamine (Asp, Asn) *status predicted
F;334,555/Binding site: N-acetylgalactosamine (Asp, Asn) *status predicted
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                                                                                                                                                                                  62 VAIDVTNVYVMGYRAGDTSYFF---NEASATEAAKYVFKDAKRKVTLPYSGNYERLQIAA 118
                                                                                                                                                                                                                           62 LALDYTNAYVYGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLEQLA 120
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                                                          RI 182
                                                                                                                                                                                                                                                                  VSFRLSGATSSSYGVFISNLRKALPYERKLYDIPLLRSTLPGSQRYALIHLTNYADETIS 61
                                                                                                                                                                                                                                                                                                          INFTTAGATVQSYTNFIRAVR-----GRLTVLP-NRVGLPINQRFILVELSNHAELSVT 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ERWAHQTREEISLGLQALTHAIS---FLRSGASNDEEKARTLIVIIQMASEAARYRYISN 207
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                                                                                               GKIRENIPLGLPALDSAITTLFYYNAN-----SAASALMVLIQSTSEAARYKFIEQQIGK 173
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43.9%;
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. Similarity 72; Conserv
Conservative
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A; Molecule type: protein A; Residues: 1-247 < KON> A; Residues: 1-247 < KON> C; Comment: This protein belongs to type I ribosomal-inactivating proteins which catal C; Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology F; 4-243/Domain: rRNA N-glycosidase homology < RNG>
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Biol. Pharm. Bull. 19, 1485-1489, 1996
A;Title: Amino acid sequences and ribosome-inactivating
A;Reference number: JC5032; MUID:97108848; PMID:8951169
A;Accession: JC5032
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C;Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 23-May-1997
C;Accession: JC5032
                                                                                                                                           C;Comment: This protein is a ribosome-inactivating protein and exhibit cytotoxic, abo C;Comment: This protein belongs to type I ribosomal-inactivating proteins which catal C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology F;22-270/product: karasurin C #status predicted <MAC>
F;24-270/product: karasurin A #status predicted <MAA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Kondo, T.; Mizukami, H.; Takeda, T.; Ogihara, Y. Biol. Pharm. Bull. 19, 1485-1489, 1996 A;Title: Amino acid sequences and ribosome-inactivating A;Reference number: JC5032; MUID:97108848; PMID:8951169
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Biol. Pharm. Bull. 20, 711-713, 1997
A;Title: Cloning and bacterial expression of a gene encoding ribosome-inactivating
A;Reference number: JC5606; MUID:97356562; PMID:9212998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Trichosanthes kirilowii var. japonica C;Date: 23-Sep-1997 #sequence_revision 23-Sep-1997 C;Accession: JC5006; JC5033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        karasurin C - Trichosanthes kirilowii var. japonica N;Contains: karasurin A
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                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein A; Residues: 22-270 < KON>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: DDBJ:AB000666; NID:g2329830; R;Kondo, T.; Mizukami, H.; Takeda, T.; Ogihara,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A; Accession: JC5606
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                                                                                                                   F;27-266/Domain: rRNA N-glycosidase homology
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                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: JC5033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62 VAIDVTNVYVMGYRAGDTSYFF---NEASATEAAKYVFKDAKRKVTLPYSGNYERLQIAA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62 LALDVTNAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLEQLA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9 INFTTAGATVQSYTNFIRAVR-----GRLTVLP-NRVGLPINQRFILVELSNHAELSVT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 VSFRLSGATSSSYGVFISNLRKALPYERKLYDIPLLRSTLPGSQRYALIHLTNYADETIS
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                    33.7%;
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Score 326; νυ ...
No. 2.2e-22;
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Pred. No. 1.8e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                             <RNG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIDN:BAA21786.1; PID:g2329831
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                                                       Length 289;
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44;

Mismatches

Indels

16;

Gaps

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A;Cross=references; GB:M98345; NID:g166296; PIDN:AAA32625.1; PID:g166297
R;Kimura, M.; Sumizawa, T.; Funatsu, G.
Biosci. Biotechnol. Biochem. 57, 166-169, 1993
A;Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, toxic A;Reference number: JC1398; MUID:93169023; PMID:7763422
A;Accession: JC1399
A;Molecule type: protein
A;Residues: 260-281,'D',283-290,'N',292-349,'PQ',352-377,'N',379-425,'M',427,'D',429-430
A;Residues: 260-281,'D',283-290,'N',292-349,'PQ',352-377,'N',379-425,'M',427,'D',429-430
A;Experimental source: seed
C;Superfamily: ricin; rRNA N-glycosidase homology
C;Keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin; F:1-250/Product: abrin-b chain A #status predicted <ACH>F:7-245/Domain: rRNA N-glycosidase homology
C;Keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin; F:260-527/Product: abrin-b chain A #status predicted <ACH>F:7-245/Domain: rRNA N-glycosidase homology
C;Keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin; F:7-245/Domain: rRNA N-glycosidase homology
C;Keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin; F:7-245/Domain: rRNA N-glycosidase homology
C;Keywords: disulfide bond; duplication; glycoprotein; glycosidase; hydrolase; lectin; F:7-245/Domain: rRNA N-glycosidase homology
C;Keywords: disulfide bond; glycoprotein; glycosidase; hydrolase; lectin; F:7-245/Domain: rRNA N-glycosidase homology
C;Keywords: disulfide bond; glycoprotein; glycosidase; hydrolase; lectin; F:7-245/Domain: rRNA N-glycosidase homology
C;Keywords: disulfide bond; glycoprotein; glycosidase; hydrolase; lectin; F:7-245/Domain: rRNA N-glycosidase homology
C;Keywords: disulfide bond; glycoprotein; glycosidase; hydrolase; lectin; F:7-245/Domain: glycoprotein; glycosidase; hydrolase; hydrolase; lectin; F:7-245/Domain: glycoprotein; glycosidase; hydrolase; lectin; F:7-245/Domain: glycoprotein; glycoprotein; glycoprotein; glycoprotein; glycoprotein; glycoprotein; glycopro
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A; Molecule type: mRNA
A; Residues: 1-527 <HUN>
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N;Contains: rRNA N-glycosidase (EC 3.2.2.22)
C;Species: Abrus precatorius (Indian licorice)
C;Date: 30-Sep-1993 #sequence_revision (01-Aug-1997 #text_change 20-Aug-1999
C;Accession: S32430; JC1399
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J. Mol. Biol. 229, 263-267, 1993
A; Title: Primary structure of three distinct isoabrins of A; Reference number: S32429; MUID:93132798; PMID:8421313
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                                                                                                                                                                                                                                                                                                                                                                                                          57
                                                                                                                                                                                                                                                                                                          61 TESIEAGIDVSNAYVVAYRAGNRSYFL---RDAPTSASRYLFTGTQ-QYSLRFNGSYIDL
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                                                       EMRTRIRYN 185
                                                                                                                                     ERLARQTRQQIPLGLQALRHAISFL----QSGTDDQEIARTLIVIIQMASEAARYRFISY 172
                                                                                                                                                                                                                   EQLAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEG 176
                                                                                                                                                                                                                                                                                                                                                                                            ELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QDQVIKFTTEGATSQSYKQFIEALRQRLTGGLIHGIPVLPDPTTLQERNRYISVELSNSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QYPIINETTAGATVQSYTNFIRAVRGRLT-----VLPNRVGLPINQRFILVELSNHA 56
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43.9%; Pred. No. 9e-22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        abrin-a precursor - Indian licorice (fragment)
N;Contains: rRNA N-glycosidase (EC 3.2.2.22)
C;Species: Abrus precatorius (Indian licorice)
C;Date: 31-Dec-1993 #sequence_revision 01-Aug-1997 #text_change 16-Jul-1999
C;Date: 31-Dec-1993 #text_change 16-Jul-1999
C;Date: 31-Dec-1993 #text_change 16-Jul-1999
C;Date: 31-Dec-1993 #text_change 16-Jul-1999
C;Date: 31-Dec-1993 #tex
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R:Evensen, G.; Mathiesen, A.; Sundan, A.
J. Biol. Chem. 266, 6848-6852, 1991
A:Title: Direct molecular cloning and expression of two distinct abrin A-chains.
A:Reference number: A39761; MUID:91201329; PMID:2016300
A:Accession: C39761
                                         A;Cross-references: GB:M98344; NID:g166294; PIDN:AAA32624.1; PID:g166295 A;Note: the coding region for the sequence shown is preceded by an ATG of A;Note: residues 1-8 were derived from the synthesized primer R;Funatsu, G.; Taguchi, Y.; Kamenosono, M.; Yanaka, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Hung, C.H.; Lee, M.C.; Lee, T.C.; Lin, J.Y.
J. Mol. Biol. 229, 263-267, 1993
A;Title: Primary structure of three distinct isoabrins determined
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C;Keywords: duplication; glycosidase; hydrolase; lectin; toxin
F;1-251/Product: abrin (clone 7.2) chain A #status predicted <ACH>
F;7-246/Domain: rRNA N-glycosidase homology <RNG>
F;74,113,195,196/Binding site: substrate (Tyr, Tyr, Glu, Asn) #stat
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A;Residues: 'M',1-251 <EV2>
A;Cross-references: EMBL:X54872; NID:g16088; PIDN:CAA38654.1; PID:g16089
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A; Residues: 1-251 <EVE>
R; Evensen, G; Mathiesen, A.; Sundan, A.
submitted to the EMBL Data Library, October 1990
A; Description: Direct molecular cloning of two distinct abrin A-chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        abrin (clone 7.2) precursor - Indian licorice (fragment)
N;Contains: rRNA N-glycosidase (EC 3.2.2.22)
C;Species: Abrus precatorius (Indian licorice)
C;Date: 21-Feb-1992 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 'E', 2-528 <HUN>
                                                                                                                                                                                                                                                                                                                                              A; Reference number: S32429; MUID:93132798; A; Accession: S32429
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A;Accession: S14471
                                    R; Funatsu,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                     A;Status: nucleic acid sequence not shown
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G.; Taguchi, Y.; Kamenosono, M.;
1. Chem. 52, 1095-1097, 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 RIR 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 HQTREQISLGLQALTHAIS---FLRSGASNDEEKARTLIVIIQMASEAARYRYISNRVGV 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       173 RVGVSIRTN 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVGIDVTNAYVVAYRAGSQSYFL---RDAPASASTYLFTGTQ-RYSLRFDGSYGDLERWA
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                                                                                                                                                                                                                                                                                                                                                                                                 PMID: 8421313
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A; McCecule type: protein
A; Residues: 89-108;154-172 < LIN>
A; Residues: 89-108;154-172 < LIN>
A; Residues: 89-108;154-172 < LIN>
A; Experimental source: seed
A; Accession: S74111
A; Molecule type: protein
A; Residues: 262-276; 'x', 278-280;329-348;369-388;399-418 < LIW>
A; Residues: 261-280;329-348;369-388;399-418 < LIW>
A; Residues: 261-280;329-348;309-348;309-348;309-348;309-348;309-348;309-348;309-348;309-348;309-348;309-348;309-348;309-348;309-348;309-348;309-348;309-348;309-348;309-348;309-348;309-348;309-348;309-348;309-348;309-348;309-348;309-348;309-348;309-348;309-348;309-348;309-348;309-348;309-348;309-348;309-348;309-348;309-34
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A;Title: The complete amino acid sequences of the B-chains of Abrin-a and Abrin-b, A;Reference number: JC1398; MUID:93169023; PMID:7763422
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A;Accession: JT0202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: protein
A;Residues: 262-297,'Y',299-426,'L',428-466,'P',468-482,'L',484-528 <CHE>
A;Residues: 262-297,'Y',299-426, 'L',428-466,'P',468-482,'L',484-528 <CHE>
R;Lin, S.H.; Chow, L.P.; Chen, Y.L.; Liaw, Y.C.; Chen, J.K.; Lin, J.Y.
Eur. J. Biochem. 240, 564-569, 1996
A;Title: Probing the domain structure of abrin-a by tryptic digestion.
A;Reference number: S74110; MUID:97008945; PMID:8856055
A;Accession: S74110
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A; Accession: S24133
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A;Note: the amino-terminal residue forms pyrrolidone carboxylic acid; therefore, R;Evensen, G; Mathlesen, A; Sundan, A.
J. Biol. Chem. 266, 6848-6852, 1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 'E', 2-251 <EVE>
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A; Accession: S14472
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A; Residues: 'ME', 2-251 <EV2>
                               Query Match
Best Local
Matches
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                                   Similarity
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Conservative
                               31.4%; Score 303.5; DB 141.1%; Pred. No. 5.5e-20
   26;
   Mismatches
                                                                      DB 1;
                                                                  Length 528;
   Indels
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   19;
Gaps
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C:Species: Luffa cylindrica (smooth loofah)
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 20-Aug-1999
C;Accession: S23519; S23113
R;Kataoka, J.; Habuka, N.; Miyano, M.; Masuta, C.; Koiwai, A.
Plant Mol. Biol. 19, 887-889, 1992
A;Title: Nucleotide sequence of cDNA encoding beta-luffin, another ribosome-inactivat A;Reference number: S23519; MUID:92353400; PMID:1643290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X62372; NID:g19149; PIDN:CAA44230.1; PID:g19150 C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology F;26-264/Domain: rRNA N-glycosidase homology <RNG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
A; Residues: 1-278 <KAT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  179 RTRIR 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 WAHQSRQQIPLGLQALTHGIS---FFRSGGNDNEEKARTLIVIIQMVAEAARFRYISNRV 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                119 LAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEM 178
                                                                                                                                     138 AAGKVREKIPLGFRAFDSAITSLFHYDS----TAAAGAFLVIIQTTAEASRFKYIEGQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   176 RVSIQ 180
193 IERIPKN 199
                                                                                                                                                                                                119 LAGNIRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARPQYIEGEM 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65 EVGIDVTNAYVVAYRAGTQSYFLRDAPSSASD-----YLFTGT-DQHSLPFYGTYGDLER 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 TLALDVTNAYVVGYRAGNSAYFFH -- PDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQ 118
                                                                                                                                                                                                                                                                                                                                     59 SYTLALDYINAYVYGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQ 118
                                                                                                                                                                                                                                                                                                                                                                                                        24 VSFSLSGADSKSYSKFITALRKALPSKEKVSNIPLLLPSASGA---SRYILMQLSNYDAK 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9 INFTTAGATVQSYTNFIRAVRGRL-----TVLPNRVGLPINQRFILVELSNHAEL
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                                                                         RTRIRYN 185
                                                                                                                                                                                                                                                                   AITMAIDVTNVYIMGYLVNSTSYFF--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 300.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. 4.6e-20;
                                                                                                                                                                                                                                                                      -NESDAKLASQYVFKGSTIVTLPYSGNYERLQN 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
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RESULT 13
JN0108
JN0108
Luffin-b - smooth loofah
C;Species: Luffa cylindrica (smooth loofah)
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 07-May-1999
C;Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 07-May-1999
C;Accession: JN0108
R;Islam, MR.; Hirayama, H.; Funatsu, G.
A;Title: Complete amino acid sequence of luffin-b, a ribosome-inactivating protein A;Reference number: JN0108; MUID:91248488; PMID:1368666
A;Accession: JN0108
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-250 cISL>
C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
F;5-246/Domain: rRNA N-glycosidase; rRNA N-glycosidase homology
Query Match

30.4%; Score 293.5; DB 2; Length 250;
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A;Accession: A32542
A;Status: preliminary
A;Stolecule type: protein
A;Residues: 21-28,'G',30,'X',32-34,'K',36-40 <RAM>
C;Function:
A;Bescription: hydrolyzes the N-glycosidic bond of a specific a C;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase homology
C;Keywords: glycoprotein; glycosidase; hydrolase; seed; toxin
F;1-20/Domain: signal sequence #status predicted <SIG>
F;1-20/Domain: signal
                                                                                                                                                                                                          F;21-267/Product: rRNA N-glycosidase alpha-luffin #status experimental <MAT> F;24-262/Domain: rRNA N-glycosidase homology <RNC> F;268-277/Domain: carboxyl-terminal propeptide #status predicted <CTP> F;488-53,97,104,225,246/Binding site: carbohydrate (Asn) (covalent) #status e F;90,179,182/Active site: Tyr, Glu, Arg #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biochem. Biophys. Res. Commun. 160, 509-516, 1989
A:Title: Characterization of a translation inhibitory protein from Luffa aegyptiaca.
A;Reference number: A32542; MUID:89246493; PMID:2719679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A:Molecule type: protein
A:Residues: 21-53'L',55,'I',57-86,'SQL',90-154,'L',156-157,'I',159-173,'L',175-209,'SL
A:Experimental source: seed
R:Ramakrishnan, S.; Enghlid, J.J.; Bryant Jr., H.L.; Xu, F.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R:Islam, M.R.; Nishida, H.; Funatsu, G. Agric. Biol. Chem. 54, 1343-1345, 1990
A;Title: Complete amino acid sequence of luffin-a, a ribosome-inactivating protein from A;Reference number: JH0202; MUID:91197482; PMID:1368623
A;Accession: JH0202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: protein
A;Residues: 21-53,'L',55,'I',57-86,'SQL',90-154,'L',156-157,'I',159-173,'L',175-209,'SL
P·Telam. M.R.: Nishida, H.; Funatsu, G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X62371; NID:g19145; PIDN:CAA44229.1; PID:g19146
R;Islam, M.R; Nishida, H.; Funatsu, G.
Agric. Biol. Chem. 54, 2967-2978, 1990
A;Title: Complete amino acid sequence of luffin-a, a ribosome-inactivati
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Plant Mol. Biol. 18, 1199-1202, 1992
A;Title: Nucleotide sequence of cDNA encoding alpha-luffin, a ribosome-inactivating prot A;Reference number: S22494; MUID:92288316; PMID:1600156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: A; Accession: $26390
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                                                                                                       Query Match
Best Local S
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                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQ 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSFSLSGADSKSYSKFITALRKALPSKEKVSNIPLLLPSASGA---SRYILMQLSNYDAK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hydrolyzes the N-glycosidic bond of a specific adenosine in 28S rRNA the rRNA N-glycosidase; rRNA N-glycosidase homology
                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enghlid, J.J.; Bryant Jr., H.L.; Xu, F.J. es. Commun. 160, 509-516, 1989
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                                                            28.4%; Score 274.5; 33.3%; Pred. No. 1.1 Live 42; Mismatches
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MUID:91248471; PMID:1368651
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6; Mismatches 57;
                                                                                                       1.1e-17
                                                                                                                                         DB 2;
                                                            61;
                                                            Indels
                                                                                                                                     Length 277;
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C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 15-Sep-2000
C;Accession: S14273; A61318; S16490; JN0628; S01670
R;HO, W.K.K.; Liu, S.C.; Shaw, P.C.; Yeung, H.W.; Ng, T.B.; Chan, W.Y.
Biochim. Biophys. Acta 1088, 311-314, 1991
A;Title: Cloning of the cDNA of Alpha-momorcharin: a ribosome inactivating protein. A;Accession: S14273; MUID:91159486; PMID:2001404
A;Accession: S14273
A;Description: hydrolyzes the N-glycosidic bond of a specific adenosine in 28S rRNA tc;Superfamily: rRNA N-glycosidase; rRNA N-glycosidase; homology C;Keywords: glycoprotein; glycosidase; hydrolase; lectin; seed; toxin F;1-18/Domain: signal sequence #status predicted <SIG> F;19-23/Domain: amino-terminal propeptide #status predicted <PRO>
                                                                                                                                                                                                                                                                                            submitted to the Brookhaven Protein Data Bank, March 1994 A; Reference number: A52385; PDB:1MOM A; Contents: annotation; X-ray crystallography, 2.16 angst: R; Huang, Q; Liu, S; Tang, Y.; Jin, S.; Wang, Y. submitted to the Brookhaven Protein Data Bank, July 1994 A; Reference number: A67089; PDB:1MRH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Note: as a lectin shows agglutinating activity for type-0 R; Montecucchi, P.C.; Lazzarini, A.M.; Barbieri, L.; Stirpe, Int. J. Pept. Protein Res. 33, 263-267, 1989
A; Title: N-terminal sequence of some ribosome-inactivating pa; Reference number: S16331; MUID: 89326691; PMID: 2753596
A; Accession: S16490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Ren, J.; Wang, Y.; Dong, Y.; Stuart, D.I. submitted to the Brookhaven Protein Data Bank, A;Reference number: A52272; PDB:1AHC
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A;Residues: 24-107,'Q',109-123,125-147,'L',149-154,'I',156-205,'I',207-208,'L',210-21
A;Experimental source: seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Biosci. Biotechnol. Biochem. 57, 1141-1144, 1993
A;Title: The complete amino acid sequence of momordin-a, a ribosome-inactivating A;Reference number: JN0628; MUID:93372485; PMID:7763984
A;Accession: JN0628
                                                                                                                                                                                                                   C; Function:
                                                                                                                                                                                                                                                     A; Contents: annotation; X-ray crystallography, 2.0 angstroms, residues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Contents: annotation; X-ray crystallography,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein A; Residues: 24-68, 'X', 70 R; Minami, Y.; Funatsu, G.
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A; Residues: 1-286 < HOW>
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F;24-269/Product: rRNA N-glycosidase alpha-momorcharin *status experimental <MAT> F;27-286/Domain: rRNA N-glycosidase homology <RNG> F;27-286/Domain: carboxyl-terminal propeptide *status predicted <CTP> F;270-286/Domain: carboxyl-terminal propeptide *status predicted <CTP> F;93,183,186/Active site: Tyr, Glu, Arg *status predicted F;250/Binding site: carbohydrate (Asn) (covalent) *status experimental
Search completed: September 16, 2003, 11:50:34 Job time : 13.1928 secs
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                                                                                                                                                                                                                            142 GKPREKIPIGLPALDSAISTLLHYDS-----TAAAGALLVLIQTTAEAARFKYIEQQIQE 196
                                                                                                                    197 R 197
                                                                                                                                                                         181 R 181
                                                                                                                                                                                                                                                               121 GNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRT 180
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 16, 2003, 11:30:32; Search time 6.59071 Seconds (without alignments) 1341.437 Million cell updates/sec

Title: Perfect score: Sequence: US-10-083-336A-4
966
1 IFPKQYPIINFTTAGATVQS.....ARFQYIEGEMRTRIRYNRRS 188

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

3333336 2254 4 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	Result No.
8615 327.5 327.3 326.3 327.5 328.3 320.5 307.5 307.5 307.5 307.5 307.5 293.5 274.5 274.5 274.5 274.5 174.1 170.1 116.5 114.1 1116.5 1114.1 1116.5 1114.1 1116.5 1114.1 1116.5 1114.1 1116.5 1114.1 1116.5 1114.1 1116.5 1114.1 1116.5 1116.5 1116.5 1116.5	Score 951
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P44755 haemophilus	Q00971 vibrio prot	P27561 saponaria o	P24153 vibrio chol	Q9bxb4 homo sapien	Q00531 hordeum vul	P75255 mycoplasma	067411 aquifex aeo	P10149 bacteriopha	P08026 bacteriopha	P25892 zea mays (m	

# ALIGNMENTS

RESULT 1  RECL_RICCO STANDARD; PRT; 576 AA. AC PO2879; PO2880; DP 13-AUG-1997 (Rel. Ol. Created) DP 13-AUG-1997 (Rel. Ol. Created) DP 13-AUG-1997 (Rel. Ol. Created) DP 13-SEP-2003 (Rel. 42. Last annotation update) DF 15-SEP-2003 (Rel. 42. Last annotation update) DR Ricing recursor [Contains: Ricin A chain (rRNA N-glycosidase) DR Ricing communis (Castor bean) CR	~ ~ ~ ~ .		. ממממט				, x x x x x x x	ж н « и и и и и и и и и и и и и
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Protein Eng. 5:775-779(1992).
-!- FUNCTION: Ricin is higly toxic to ani
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Day P.J., Ernst S.R.,
Molina-Svinth M.C., R
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pauptit R.A.;
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*Analysis of several key active site residues of ricin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MUTAGENESIS
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galactopyranoside moieties.

CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at specific adenosine on the 28s rrna.

SUBUNIT: Disulfide-linked dimer of A and B chains.

SUBUNIT: The B chain is composed of two domains, each domain consists of 3 homologous subdomains (alpha, beta, gamma).

PTM: THE MAJOR A-CHAIN IS GLYCOSYLATED ONLY IN POSITION 45 AND MINOR A-CHAIN IS GLYCOSYLATED ALSO IN POSITION 271.

SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Ricin is highy toxic to animal cells and to a less extent to plant cells. The A chain is responsible for inhibiti protein synthesis through the catalytic inactivation of 60S ribosomal subunits. It acts as a glycosidase that removes a specific adenine residue from an exposed loop of 28S ribosomal RNA. As this loop is involved in the binding of elongation factors, the modified ribosomes are unable to support protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             synthesis. The A chain can inactivate a few thousand ribosomes per minute, thus inactivating them faster than the cell can make new ones. A single A-chain molecule can therefore kill an animal cell. The B chain binds to cell receptors and facilitates the entry into the cell of the A chain; B chains are also responsible for cell agglutination (Lectin activity). It binds to beta-D-
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f ricin B-chain at 2.5-A resolution.";
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SMART; SM00458; RICIN; 2.
PROSITE; PS50231; RICIN_BLIECTIN; 2.
PROSITE; PS00275; SHIGA_RICIN; 1.
Plant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
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InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Contains 2 ricin B-type lectin domains.
-!- CAUTION: REF.4 AND REF.5 SEQUENCES HAVE A HIGH NUMBER OF CONFLICTS
WITH THE SEQUENCE TRANSLATED FROM DNA (REF.1, REF.2 AND REF.3).
-!- DATABASE: NAME-Protein Spotlight;
                                                                                                                                                                                                                                                                                                                                           PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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A24041; RLCSD.
2AAI; 31-JAN-94.
                                                                                                                                                                                                                                                                                                 PF00652; Ricin_
PF00161; RIP; 1
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X52908; CAA37095.1;
X02388; CAA26230.1;
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Best Local Similarity
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01-JAN-1988 (Rel. 06, Last sequence update)
28-FEB-2003 (Rel. 41, Last annottation update)
28-FEB-2003 (Rel. 41, Last annottation update)
Agglutinin precursor (RCA) [Contains: Agglutinin A chain (rRNA N-glycosidase) (EC 3.2.2.2); Agglutinin B chain].
Ricinus communis (Castor bean).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Malpighiales; Euphorbiaceae; Ricinus.
                                                                                                                                                                  MEDLINE-80178723; PubMed-6768555;
Lin T.T.-S., Li S.S.-L.;
"Purification and physicochemical properties of ricins and "Purification and Ricinus communis.";
Eur. J. Biochem. 105:453-459(1980).
--I- CAMALYTIC ACTIVITY: Endobydrolysis of the N-glycosidic specific adenosine on the 285 rRNA.
--I- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE R INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY.
--I- SIMILARITY: Contains 2 ricin B-type lectin domains.
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                                             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE=86059449; PubMed=2999130;

Roberts L.M., Lamb F.I., Pappin D.J.C.,

"The primary sequence of Ricinus communi
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                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 303-337.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    OF 303-564.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Yoshioka Y., Funatsu G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
AAA33869.1;
AAB22584.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  260:15682-15686(1985).
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94.9%;
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No. 2.2e-80;
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                                                            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lord J.M
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Best Local
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HSSP; P02879; 1BR6.
GlycoSuiteDB; P06750; ...
InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
InterPro; IPR001574; RIP.
Pfam; PF00652; Ricin_B_lectin; 6.
Pfam; PF00161; RIP; 1.
PRINTS; PR00396; SHIGARICIN.
SMART; SM00458; RICIN; 2.
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CARBOHYD
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      Ribosome-inactivating protein alpha-trichosanthin (rRNA N-glycosidase) (EC 3.2.2.2) (Alpha-TCS).
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REPEAT
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REPEAT
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                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                             FOYIEGEMRTRIRYNRRS
                                                                                                         FQYIEGEMRTRIRYNRRS
                                                                                                                              GNYDRLEQL-GGLRENIELGTGPLEDAISALYYYSTCGTQIPTLARSFMVCIQMISEAAR
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kirilowii
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                                                       STANDARD;
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                       Last sequence update)
Last annotation updat
                                        Created)
(Mongolian
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N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
F-> T (IN REF. 2).
N-> D (IN REF. 2).
R-> G (IN REF. 2).
R-> T (IN REF. 2).
R-> V (IN REF. 2).
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BY SIMILARITY.
N-LINKED (GLCNA
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2-ALPHA.
2-BETA.
2-GAMMA.
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RICIN B-TYPE
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N B-TYPE LECTIN :
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EMBL; M34858; A
EMBL; J05434; A
PIR; JT0566; RI
PDB; 1MT, 07-F
PDB; 1MT, 07-F
PDB; 1TCS; 10-J
PDB; 1J4G; 28-J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-Maximowicz; TISSUE-Leaf;
MEDLINE-90256790; PubMed-2341400;
Chow T., Feldman R.A., Lovett M., Piatak M.;
"Isolation and DNA sequence of a gene encoding alpha-trichosanthin, a type I ribosome-inactivating protein.";
J. Biol. Chem. 265:8670-8674(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang Y.,
Tian G.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene
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                                                                                                                                                                                                                                                                                    the European Bloinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                                                                                                         This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        depurinating mechanism of two ribosome-inactivating proteins. Biochem. J. 309:285-298(1995).
-i- FUNCTION: TRICHOSANTHIN IS AN ABORTION-INDUCING PROTEIN. J. CAPABLE OF INHIBITING HIV-1 INFECTION AND REPLICATION. IT INACTIVATES EUKARYOTIC 60S RIBOSOMAL SUBUNITS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wu P., Hwang K., Piatak M.; "Primary amino acid sequence of alpha-trichosanthin and molecular models for abrin A-chain and alpha-trichosanthin."; J. Biol. Chem. 265:8665-8669(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 24-270.
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MEDLINE=91153657;
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MEDLINE=94344957; PubMed=8066085;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Scientific evaluation of Tian Hua Fen (THF): history, chemistry and application.";
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Shaw P.C., Yung M.H., Zhu R.H., Ho W.K.K., Ng T.B., Y
"Cloning of trichosanthin cDNA and its expression in
                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Huang Q., Liu S., Tang Y., Jin S., Wang Y.;
"Studies on crystal structures, active-centre geometry and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95344383; PubMed=7619070;
                                                                                                                                                                                                                                                                                                                                                                               between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at especific adenosine on the 28S rRNA.
SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F., Fu Z., Chen M., Lin Y., Pan K.; ucture of trichosanthin at 1.88-A resolution.";
                                                                                                                                                                                                                                                                                                                                                                            SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Appl. Chem. 58:789-798(1986).
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     07-FEB-95.
07-FEB-95.
10-JUL-95.
28-JAN-03.
                                                                                                                                                                                                                                  email to license@isb-sib.ch).
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AAA34206.1; -.
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n Escherichia
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PDB; 1QD2; 24-APR-00.
InterPro; IPR001574; RIP.
Pfam; PF00161; RIP; 1.
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                                                                                                                                                                                                                                                                 Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase; Toxin; Signal; 3D-structure.
                                                                                                                                                                                                                                                                         PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN;
            SEQUENCE
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           MISSING IN MATURE PROTEIN.
BY SIMILARITY.
IPLL -> LPLI (IN REF. 4).
MISSING (IN REF. 4).
I -> L (IN REF. 4).
V -> VDAGLERNAVL (IN REF. 4
KI -> GL (IN REF. 4).
K -> S (IN REF. 4).
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Score 336; DB 1
Pred. No. 7e-24;
                                                                                                                                                                                                        Q -> T (IN REF. 4).
S -> T (IN REF. 2).
                                                                                                                                                                                                                 WS -> LWL (IN REF. 4).
                                                                                                                                                                                                                                                          RIBOSOME-INACTIVATING PROTEIN ALPHA
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             5CE09BB630575BB9 CRC64;
                                                                                                                                                                                                ING (IN REF. 4)
M (IN REF. 2).
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Query Match Best Local S Matches 72

Similarity

34.8%;

Conservative

Mismatches

49;

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Gaps

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Length 289; Indels

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THE RESULT 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-DEC-1992 (Rel. 24, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Abrin-c precursor [Contains: Abrin-c A chain (rRNA N-glycosidase)
(EC 3.2.2.2); Abrin-c B chain].
Abrus precatorius (Indian licorice) (Crab's eye).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosid
eurosids I; Fabales; Fabaceae; Papillonoideae; Abreae; Abrus.
                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                      EMBL; X55667; CAA39202.1;
PIR; S16022; S16022.
HSSP; P11140; 1ABR.
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                      PRINTS; PR00396; SHIGARICIN.
SMART; SM00458; RICIN. 2.
PROSITE; PS50231, RICIN. LECTIN; 2.
PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=3816;
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                                                                                                                              InterPro; IPR000772; Ricin_B_1
InterPro; IPR01574; RIP.
Pfam; PF00552; Ricin_B_lectin;
Pfam; PF00161; RIP; 1.
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synthesis inhibitor;
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  Toxin; Repeat;
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RESULT 5
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Best Local S
Matches 82
                                                                                                                                                                                                                                               P24478;

D1-MAR-1992 (Rel. 21, Created)

15-DEC-1998 (Rel. 37, Last sequence update)

26-FEB-2003 (Rel. 41, Last annotation update)

Ribosome-inactivating protein karasurin precursor (rRNA N-glycosidase) (EC 3.2.2.2).

Trichosanthes kirilowii (Mongolian snake-gourd).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trichosanthes kirilowii (cucurbitaceae; Trichosanthes.)
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                                                                                     Mizukami H., Iida K., Kondo T., Ogihara "Cloning and bacterial expression of a inactivating proteins, karasurin-A and kirilowii var. japonica.";
                                                                                                                                          TISSUE=Root tuber;
MEDLINE=97356562; PubMed=9212998;
Mizukami H., Iida K., Kondo T., O
[2]
SEQUENCE OF 24-270.
SEQUENCE OF 24-270.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIPS_TRIKI
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                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                   Pharm. Bull.
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82; Conser
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                                                                   japonica.";
ull. 20:711-713(1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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RICIN B-TYPE LECTIN 1.
RICIN B-TYPE LECTIN 2.
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BY SIMILARITY
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LINKER PEPTIDE (BY SIMILARITY).
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                                                                                                                                            Ogihara Y.;
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                                                                                                        karasurin-C,
                                                                                                                          gene encoding ribosome-
                                                                                                                                                                                                                                                                                             Embryophyta; Tracheophyta
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                                                                                                                                                                                                                                                                                 Rosidae;
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RESULT 6
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ID ABBRE
ID ABBRE
AC Q06C
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DT 15-L-
DT 28-F
DT 28-F
DT 28-F
OC EUKA
OC EUKA
OC SPERT
OC WCBIRR
RN SEGU
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Best Local
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                                                  ABRB_ABRPR STANDARD; PRT; 527 AA.

060677; P81374;

15-DEC-1998 (Rel. 37, Created)

15-DEC-1998 (Rel. 37, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)

Abrin-b precursor [Contains: Abrin-b A chain (rRNA N-glycosidase)

Abrus precatorius (Indian licorice) (Crab's eye),

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; endicotyledons; core endicots; Rosid.

Spermatophyta; Magnollophyta; endicotyledons; Abreae; Abrus.
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                                     NCBI_TaxID=3816;
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FUNCTION: ABORTION-INDUCING PROTEIN. IT INACTIVATES EUKARYOTIC 60S RIBOSOMAL SUBUNITS.
CATALYTIC ACTIVITY: Endchydrolysis of the N-glycosidic bond at specific adenosine on the 28S rRNA.
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JU0393; JU0393.
, P09989; IMRJ.
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complete amino acid sequence of an abortifacient protein,
                                                                                                                                                                                                                                                                                                                                               181
                                                                                                                                                                                                                                                                                                                 197
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183
289 AA;
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Pred. No. 5
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SMART; SM00458; RICIN; 2.
PROSITE; PS50231; RICIN_B LECTIN;
PROSITE; PS00275; SHIGA_RICIN; 1.
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Pfam; PF00161; RIP; 1.
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InterPro; IPR001574; RIP.
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INTERCHAIN (BY SIMILARITY).
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RICIN B-TYPE LECTIN
RICIN B-TYPE LECTIN
                                                                                   PYRROLIDONE CARBOXYLIC
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Biosci. Biotechnol. Biochem. 57:166-169(1993).

-i - FUNCTION: THE A CHAIN IS REPONSIBLE FOR INHIBITING PROTEIN
SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL
SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RRNA.
ABRIN-A IS MORE TOXIC THAN RICIN.
-i- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT
FORCILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
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-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at specific adenosine on the 28S IRNA.
-!- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.
-!- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETTA, GAMMA).
-!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hung C.-H., Lee M.-C., Lee T.C., Lin J.-Y.;
"Primary structure of three distinct isoabrins determined by cDNA sequencing. Conservation and significance.";
J. Mol. Biol. 229:263-267(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY. -!- SIMILARITY: Contains 2 ricin B-type lectin domains.
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"The complete amino acid sequences of the B-chains of abrin-a and abrin-b, toxic proteins from the seeds of Abrus precatorius.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93132798; PubMed=8421313;
                                                                            ant defense; Hydrolase; Protein synthesis inhibitor; Toxin; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
Pyrrolidone carboxylic ABRIN-B A CHAIN.
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Bryonia diolca (Red bryony).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids I; Cucurbitales; Cucurbitaceae; Bryonia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Siegall C.B., Gawlak S.L., Marquarc "Bryodin 2 a ribosome-inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Ribosome-inactivating protein bryodin II precursor (rRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BRYDI
                                                                                                                                                                Bioconj. Čhem. 5:423-429(1994).
-I- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1,
                                                                                                                                                                                                                                            "Characterization of ribosome-inactivating proteins isolated Bryonia dioica and their utility as carcinoma-reactive
                                                                                                                                                                                                                                                                                                                          MEDLINE=95151812; PubMed=7849072;
Siegall C.B., Gawlak S.L., Chace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bryonia dioica.
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                                                                                                                                                                                                                                                                                                                                                                                TISSUE-Root
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent number US5597569,
                                                                                                                                                                                                                     immunoconjugates."
                                                                                 PROTEIN SYNTHESIS IN ANIMAL CELLS (BY SIMILARITY). CATALYTIC ACTIVITY: Endohydrolysis of the N-glycos specific adenosine on the 28S rRNA.
                                                           SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING
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                                 1 RIP SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                          D., Wolff E.A.,
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P33183; P33184; P93542;
01-OCT-1993 (Rel. 27, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Nigrin b precursor (Agglutinin V) (SNAV) [Contains: Nigrin b A chain
(FRNA N-glycosidase) (EC 3.2.2.22); Nigrin b B chain].

Sambucus nigra (European elder).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACT_SITE CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAMNI
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HSSP; P09989; 1MRJ.
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or send an email to license@isb-sib.ch).
                          Girbes T., Citores L., Ferreras J.M., Rojo M.A., Igles Munoz R., Arias F.J., Calonge M., Garcia J.R., Mendez "Isolation and partial characterization of nigrin b, a novel type 2 ribosome inactivating protein from the benigra L.";
                                                                                                                                                                                                                                                                                                                                                               Spermatophyta; Magnoliophyta; eudicotyledons;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00396; SHIGARICIN. PROSITE; PS00275; SHIGA_RICIN;
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Pfam; PF00161; RIP; 1.
                                                                                                                                                                               Van Damme E.J., Barre A., Rouge P., Van Leuven F., Peumans W.J.; "Characterization and molecular cloning of Sambucus nigra agglutinin (nigrin b), a GalNAc-specific type-2 ribosome-inactivating protein from the bark of elderberry (Sambucus nigra)."; Eur. J. Biochem. 237:505-513(1996).
              Plant Mol.
                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4202;
                                                                                                                                                                                                                                                                                                                                                     Asteridae;
                                                                                                                MEDLINE=94003077; PubMed=8400135;
                                                                                                                                 TISSUE=Bark
                                                                                                                                                 SEQUENCE OF 26-49 AND 298-321.
                                                                                                                                                                                                                                                                                      TISSUE-Bark
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                                                                                                                                                                                                                                                                   MEDLINE=96215449; PubMed=8647092;
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282 A
                 Biol.
                                                                                                                                                                                                                                                                                                                                                     campanulids; Dipsacales; Adoxaceae;
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                                                 nigrin b, a non-toxic from the bark of Samb
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PROSITE; PS50231; RICIN_B_LECTIN;
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InterPro; IPR001574;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SÜBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS. SIMILARITY: IN THE NERMINAL SECTION; BELONGS TO THE INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY. SIMILARITY: Contains 2 ricin B-type lectin domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN SYNTHESIS BUT DOES NOT AFFECT PLANT NOR BACTERIAL PROTEIN SYNTHESIS. THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RRNA. THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      specific adenosine on the
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114 DRLEQLAGNIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQY
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SM00458; RICIN; 2.
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                                                                 NGNTVTLAVDVTNLYVVAFSGNANSYFF-----KDATEVQKSNLFVGTKQN-TLSFTGNY
                                                                                                          AELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAI - - THLFTDVQNRYTFAFGGNY
                                                                                                                                                       YPSVSFNLDGAKSATYRDFLSNLRKTVATGTYEVNGLPVLRRESEVQVKSRFVLVPLTNY
                                                                                                                                                                                             YPIINFTTAGATVQSYTNFIRAVR-----GRLTVLPNRVGLPINQRFILVELSNH
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2-BETA.
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between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There as

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P33185; O9S8I9;
01-OCT-1993 (Rel. 27, Created)
16-OCT-2001 (Rel. 40, Last seq
28-FEB-2003 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bryonia dioica (Red bryony).
Eukaryota; Viridiplantae; Streptophyta; Embryoph;
Spermatophyta; Magnoliophyta; eudicotyledons; coi
eurosids I; Cucurbitales; Cucurbitaceae; Bryonia
                                                                                                                                                                                                                              PROTEIN SYNTHESIS IN ANIMAL CELLS.
-I- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
                                                                                                                                                                                                                                                                                                    immunoconjugates.";
Bioconj. Chem. 5:423-429(1994).
-!- FUNCTION: RIBOSOME-INACTIVATING PROTEIN OF TYPE 1, INHIBITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ribosome-inactivating protein (EC 3.2.2.22) (BD1).
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Montecucchi P.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Molecular, biological, and preliminary structure combinant bryodin 1, a ribosome-inactivating Bryonia diolog.":
This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                       -!- BIOTECHNOLOGY: Especially useful as
                                                                                                                                                                                                                                                                                                                                                                                        Bryonia dioica and
                                                                                                                                                                                                                                                                                                                                                                                                                                         Marquardt H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Siegall C.B., Gawlak S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=95151812; PubMed=7849072;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 24-43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "N-terminal sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 24-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent number US5541110, 30-JUL-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Siegall C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gawlak S.L., Neubauer M., Klei H.E., Chang C.Y.Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                   "Characterization of ribosome-inactivating
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                                                                         pharmacological applications as it has low toxicity in rats and mice but is potent once inside target cells.
SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
                                                                                                                                                                             PTM: APPEARS TO UNDERGO PROTEOLYTIC CLEAVAGE IN PRODUCE A SHORTER PROTEIN.
                                                   TYPE 1 RIP SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                or ribosome-inactivating proteins isolated their utility as carcinoma-reactive
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es. 33:263-267(1989).
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                           Similarity
                                                                                                                                                                                                                                                       PS00275; SHIGA_RICIN; 1.
LALDYTNAYYVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLEQLA 120
        VSFRLSGATTTSYGVFIKNLREALPYERKYYNIPLLRSSISGSGRYTLLHLTNYADETIS
                                                                                                                                                                                                                                                                  IPR001574; RIP
               INFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPI-----NQRFILVELSNHAELSVT
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                                                                                                                                                                                                                                               Multigene
                                                                                                                                                                                                                                               Protein synthesis inhibitor; Hydrolase; Toxin; multigene family; Glycoprotein; Signal.
                                                                                                                                                                                                                                                               RIP;
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                                               31.6%;
                                       31788 MW;
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N-LINKED (GLCNAC. . .)
E->K: REDUCES ACTIVITY
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                                                                                                                                                                                                                               RIBOSOME-INACTIVATING PROTEIN BRYODIN I. MISSING IN MATURE PROTEIN.
BY SIMILARITY.
                       Score 305; DB 1;
Pred. No. 5.2e-21;
5; Mismatches 56
                                       E966CD9C031A42DB CRC64;
                               Length 290;
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RX MEDLINE-9533188; PUNDED-180980;

RA Tabirov T.H., Lu T.-H., Liaw Y.-C., Chen Y.-L., Lin J.-Y.;

RA Tabirov T.H., Lu T.-H., Liaw Y.-C., Chen Y.-L., Lin J.-Y.;

RT "Crystal structure of abrin-a at 2.14 A.";

RT OCCUPANTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALTTIC INACTIVATION OF 60S RIBOSOWAL CONSTRUCTION: THE A CHAIN IS RESPONSIBLE FROM POSITION 4,324 OF 28 S RRNA.

CONSTRUCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACTLITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.

C-!- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAINS.

C-!- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS, EACH DOMAIN CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).

C-!- SIMILARITY: IN THE N-TERMINAL SECTION; BELONGS TO THE RIBOSOME-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL 1989 (Rel. 11, Created)
01-JUL 1989 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Abrin-a precursor [Contains: Abrin-a A chain (rRNA N-glycosid (EC 3.2.2.2); Abrin-a B chain].
Abrus precatorius (Indian licorice) (Crab's eye).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; eurosids I; Fabales; Fabaceae; Papilionoideae; Abrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hung C.-H., Lee M.-C., Lee T.C., Lin J.-Y.;
"Primary structure of three distinct isoabrins sequencing. Conservation and significance.";
J. Mol. Biol. 229:263-267(1993).
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01-JUL-1989 (Re
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Chen Y.-L., Chow L.-P., Tsugita A., Lin J.-Y.;
"The complete primary structure of abrin-a B chain.";
FEBS Lett. 309:115-118(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Seed;
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We Plant defense; Hydrolase; Pytrotein synthesis inhibitor; Toxin; Repeat; KW Plant defense; Hydrolase; Pytrotein synthesis inhibitor; Toxin; Repeat; KW Glycoprotein; Lectin; 3D-structure; Pytrolidone carboxylic acid.
FT CHAIN 252 261 LINKER PEPTIDE.
FT CHAIN 262 528 ABRIN-A B CHAIN.
FT DOMAIN 262 528 ABRIN-A B CHAIN.
FT DOMAIN 403 527 RICIN B-TYPE LECTIN 1.
FT REPEAT 369 401 FRICIN B-TYPE LECTIN 2.
FT REPEAT 453 492 RICIN B-TYPE LECTIN 2.
FT REPEAT 453 493 1-ALPHA.
FT REPEAT 454 495 2-ALPHA.
FT REPEAT 455 288 2-CAMMA.
FT REPEAT 455 288 2-CAMMA.
FT REPEAT 456 305 BY SIMILARITY.
FT REPEAT 457 269 INTERCHAIN (BY SIMILARITY).
FT DISULFID 286 305 BY SIMILARITY.
FT DISULFID 329 346 BY SIMILARITY.
FT DISULFID 456 473 BY SIMILARITY.
FT DISULFID 456 473 BY SIMILARITY.
FT CARBOHYD 401 401 WILLIARITY.
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . . ).
FT CONFLICT 298 298 N SIMILARITY (GLCNAC. . . ).
FT CONFLICT 427 427 M -> Y (IN REF. 4).
FT CONFLICT 483 483 Y -> P (IN REF. 4).
FT CONFLICT 483 483 Y -> L (IN REF. 4).
                                                                                                                                                                                                                                                                                                                   EMBL; M98344; AAA32624.1; ALT_INIT.
EMBL; X54872; -; NOT_ANNOTATED_CDS.
PIR; S32429; TZLSA.
PDB; 1ABR; 07-FEB-95.
InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
Pfam; PF00652; Ricin_B_lectin; 6.
Pfam; PF00652; Ricin_B_lectin; 6.
Pfam; PF00161; RIP; 1.
PROMITS; PR00396; SHIGARICIN.
SMART; SM00458; RICIN_B_LECTIN; 2.
PROSITE; PS00275; SHIGA_RICIN; 1.
PROSITE; PS00275; SHIGA_RICIN; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             INACTIVATING PROTEIN FAMILY. TYPE 2 RIP SUBFAMILY. SIMILARITY: Contains 2 ricin B-type lectin domains.
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         Similarity
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  Score 303.5;
Pred. No. 1.5e
26; Mismatches
         .5e-20;
               DB 1;
  Indels
              Length
               528;
  19;
 Gaps
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Islam M.R., Hirayama H., Funatsu G.;
Islam M.R., Hirayama H., Funatsu G.;
"Complete amino acid sequence of luffin-b, a ribosome-inactivating protein from sponge gourd (Luffa cylindrica) seeds.";
Agric. Biol. Chem. 55:229-238(1991).
-!- CATALYIC ACTIVITY: Endobydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Luffa cylindrica (Smooth loofah) (Sponge gourd).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eu
eurosids I; Cucurbitales; Cucurbitaceae; Luffa.
                                                                                                                                                                                                                                                                                                                                                                  PIR; JN0108; JN0108.

HSSP; P16094; 1AHC.
InterPro; IPR001574; RIP.
InterPro; IPR001574; RIP.
Pfam; PF00161; RIP; 1.
PRINTS; PR00396; SHIGARICIN.
PROSTIE; PS00275; SHIGARICIN; 1.
Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ribosome-inactivating protein luffin-B (TRNA'N-glycosidase) (EC 3.2.2.22).
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01-AUG-1991
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01-AUG-1991 (Rel. 19, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EVGIDVTNAYVVAYRAGTQSYFLRDAPSSASD----YLFTGT-DQHSLPFYGTYGDLER 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IKFSTEGATSQSYKQFIEALRERLRGGLIHDIPVLPDPTTLQERNRYITVELSNSDTESI 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFTTAGATVQSYTNFIRAVRGRL-----TVLPNRVGLPINQRFILVELSNHAELSV 60
                                                                                                                                             SVTLALDYTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQ 118 ::|:|:|| | : |||:||:
                               RTRIRYN 185
                                                                                            LAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEM 178
                                                                                                                          AITMAIDVTNVYIMGYLVNSTSYF---ANESDAKLASQYVFKGSTLVTIPYSGNYERLQN 116
                                                                                                                                                                                          VSFSLSGADSKSYSKFITALRKALPSKEKVSNIPLLLPSASGA---SRYILMQLSNYDAK 59
                                                            AAGKIREKIPLGFRALDSALTSIFHYDS-----TAAAAAFLVILQTTAEASRFKYIEGQI 171
                                                                                                                                                                                                                        INFTTAGATVQSYTNFIRAVRGRL------TVLPNRVGLPINQRFILVELSNHAEL 58
                                                                                                                                                                                                                                                                                                                      160
250 AA;
                                                                                                                                                                                                                                                        Conservative
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27293 MW;
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ALD DESCRIPTION OF THE PROPERTY OF THE PROPERT
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16-OCT-2001
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inactivating protein from Cucumis figarei.";
Plant Biotechnol. 17:337-340(2000),
-:- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28s rrna.
-:- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
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16-OCT-2001 (Rel. 40, Last sequence up
28-FEB-2003 (Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (EC 3.2.2.22).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00161; RIP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamada T., Ohki S.T., Osaki T., ^{\circ}Cloning and analysis of a cDNA coding a putative ribosome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                        145
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                                                  182 IRYNR 186
                                                                                                                                                        122 NLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRTR 181
                                                                                                                                                                                                                                                   62 LALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAG
:|:||| | : | | : | : : | : : |
                                                                                                                                                                                                                 88 MAVDVTNVYIMGYLVNGTSYFF---NETDAQLASKFVFQGTKSITLPYSGNYQKLQSVAR
                                                                                                                                                                                                                                                                                                                          28 VKFSLLGSNHKSYSKFITSMRNALPNAGDIYNIPLLVPSISGSRRYILMQLSNYEGNTIT
                                                                                                                                                                                                                                                                                                                                                                             9 INFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPI-----NQRFILVELSNHAELSVT
                                                                                                                                                                                                                                                                                                                                                                                                                                     60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
ISVSK
                                                                                                        KERDSIPLGFMALDSAISTLYYYDSRSAPI---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein synthesis inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                     46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 281.5;
Pred. No. 7.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                           AFLVLIQTTAEAARYKYIEKQIIDR
                                                                                                                                                                                                                                                                                                                                                                                                                                     64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 286;
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RESULT

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RIPA, LUFCY
ID RIPA, LUFCY
OO 00465
OF 001-DEC
DT 01-DEC
DT 01-DEC
DT 28-FEB
DE RIBOSO
DE N-91990
OC Sperma
OC EUKARY
OC SPERMA
OC HORSUE
RY MEDLIN
RA KATAON
RA KATAON
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RA KATAON
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C Q00465;
T Q1-DEC-1992 (Rel. 24, Created)
T Q1-DEC-1992 (Rel. 24, Last sequence update)
T Q1-DEC-1992 (Rel. 24, Last sequence update)
DT Q8-FEB-2003 (Rel. 41, Last annotation update)
DE Ribosome-inactivating protein luffin-alpha precursor (rRN Palycosidase) (EC 3.2.2.22).
DE N-glycosidase) (EC 3.2.2.22).
OS Luffa cylindrica (Smooth loofah) (Sponge gourd).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudic eurosids I; CCCurbitales; Cucurbitaceae; Luffa.
                    RESULT 14
RIP1_MOMCH
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RIP1_MOMCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIINE-92268316; PubMed=1600156;
Kataoka J., Habuka N., Miyano M., Masuta C., Koiwai A.;
"Nucleotide sequence of cDNA encoding alpha-luffin, a ribosome-inactivating protein from Luffa cylindrica.";
Plant Mol. Biol. 18:1199-1202(1992).
-!- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 285 rRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; X62371; CAA44229.1; -. PIR; S22494; S22494. HSSP; P16094; IAHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way use by and this statement is not removed. Usage by and for commercial modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant defense; Antiviral; Protein synthesis inhibitor; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001574; RIP.
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                                                                                                                                                                                 135
                                                                                                                                                                                                                        118
                                                                                                      190
                                                                                                                                                                                                                                                              78
                                                                                                                                                                                                                                                                                               58 LSVTLALDVINAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLE
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                                                                                                                                                                                                                                                                                                                                                                                 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                         MRTRIRYNR 186
                                                                                                                                                                               TAAGKIREKIPLGFPALDSAITTLFHYDS-----TAAAAAFLVIIQTTAEASRFKYIEGQ
                                                                                                                                                                                                                                                            KAITVAVDVINVYIMGYLVNSTSYFF---NESDAKLASQYVFKGSTIVTLPYSGNYEKLQ
                                                                                                    IIERISKNO
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                                                                                                                                                                                                                                                                                                                                           VRFSLSGSSSTSYSKFIGDLR---KALPSN-GTVYNITLLLSSASGASRYTLMTLSNYDG
                                                                                                                                                                                                                                                                                                                                                                                 INFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPIN------QRFILVELSNHAE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179
277 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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  STANDARD;
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277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 274.5; DB 1;
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  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EA17FC27998C25AC CRC64;
  286
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                                                                                                                                                                                                                                                                                                                                                                                                                      1.2e-18;
nes 61;
A
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                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 277;
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                                                                                                                                                                                                                                                                                                                                                                                                                        23;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Huang Q., Liu S., Tang Y., Jin S., Wang Y.;

"Studies on crystal structures, active-centre geometry and depurinating mechanism of two ribosome-inactivating proteins.";

Biochem. J. 309:285-298(1995).

-i- CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28S rRNA.

-i- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P16094; P24697;
O1-APR-1990 (Rel. 14, Created)
O1-APR-1992 (Rel. 21, Last sequence update)
O1-MAR-1992 (Rel. 21, Last sequence update)
O1-MAR-1992 (Rel. 42, Last annotation update)
I5-SEP-2003 (Rel. 42, Last annotation I precursor (rRNA
R1bosome-inactivating protein momordin I precursor (rRNA
N-91ycosidase) (EC 3.2.2.2) (Alpha-momorcharin) (Alpha-MMC).
Momordica charantia (Bitter gourd) (Balsam pear).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Momordica.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ren J., Wang Y., Dong Y., Stuart D.I.; "The N-glycosidase mechanism of ribosome-inactivating implied by crystal structures of alpha-momorcharin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Guillemot J.C., Ferrara P., Bolognesi A., Cenini P., Stirpe i "Trichokirin, a ribosome-inactivating protein from the seeds Trichosanthes kirilowii Maximowicz. Purification, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=91159486; PubMed=2001404;
HO W.K.K., Liu S.C., Shaw P.C., Yeung H.W., Ng T.B., Chan W.Y.;
"Cloning of the cDNA of alpha-momorcharin: a ribosome inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-95344383; PubMed-7619070;
Huang Q., Liu S., Tang Y., Jin S., Wang Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS). MEDLINE=94356447; PubMed=8075985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     characterization and use for preparation Eur. J. Biochem. 176:581-588(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              x-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Husain J., Tickle I.J., Wood S.P.; "Crystal structure of momordin, a typrotein from the seeds of Momordica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         x-ray CrysTallography (2.16 ANGSTROMS).
MEDLINE-94192822; PubMed-8143869;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Casellas P., Dussossoy D., Falasca A.I., Barbieri L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=89005108; PubMed=3262509;
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                                                                                                                                                                                           TYPE
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2:7-16(1994).
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Lazzarini A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  some ribosome-inactivating proteins.";
es. 33:263-267(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a type I ribosome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteins
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or send an email to license@isb-sib.ch).

S14273;

X57682; CAA40869.1;

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                                                                                                                                       Query Match
Best Local S
Matches 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00396; SHIGARICIN.

PROSITE; PS00275; SHIGA_RICIN; 1.

Plant defense; Protein synthesis inhibitor; Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GlycoSuiteDB; p16094; -. Interpro; IPR001574; RIP. Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                            SEQUENCE
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85 VAVDVTNVYIMGYLADTTSYFF---NEPAAELASQYVFRDARRKITLPYSGNYERLQIAA 141
                62 LALDVTNAYVVGYRAGNSAYFFHPDNQEDAE-AITHLFTDVQNRYTFAFGGNYDRLEQLA 120 :|:||| |::|| ::| : ||:||:||: |
                                                                                                         9
                                                                                                                                         Similarity
63; Conser
                                                                   VSFRLSGADPRSYGMFIKDLRNALPFREKVYNIPLLLPSVSGAGRYLLMHLFNYDGKTIT
                                                                                                   INFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPI-----NQRFILVELSNHAELSVT
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22-JUN-94.
22-JUN-94.
31-MAY-94.
07-FEB-95.
                                                                                                                                         Conservative
                                                                                                                                                                                                                                                          31532 MW;
                                                                                                                                                     28.3%; Score 273; 34.8%; Pred. No. 4
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/FTId-CAR_000082.
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                                                                                                                                                                                                         E1B013ABEBC216CF CRC64;
                                                                                                                                       Mismatches
                                                                                                                                                     4.6e-18;
                                                                                                                                                                       DB 1;
                                                                                                                                                                     Length 286;
                                                                                                                                       Indels
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                                                                                                                                     Gaps
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Дb
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RIP2_MOMBA
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P29339;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ribosome-inactivating protein momordin II precursor (rRNA
N-glycosidase) (EC 3.2.2.2).
Momordica balsamina (Bitter gourd) (Balsam pear).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Momordica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001574; RIP.
Pfam; PF00161; RIP; 1.
PRINTS; PR00396; SHIGARICIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S25560; S25560.
PDB; 1CF5; 07-JUN-99.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ortigao M., Better M.;
"Momordin II, a ribosome inactivating protein from Momordica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=93027170; PubMed=1408771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lant defense; Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          samina, is homologous to other plant proteins.";
leic Acids Res. 20:4662-4662(1992).
CATALYTIC ACTIVITY: Endohydrolysis of the N-glycosidic bond at one specific adenosine on the 28s rRNA.
SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
TYPE 1 RIP SUBFAMILY.
122 NLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRTR : | | | | | | | | : | | : | : | | : | | | : | | : | : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 GNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRT 180
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                                                                                                   85
                                                                                                                                                            62
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                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                l Similarity
63; Conserv
                                                                                                VAIDVTNVYVVAYRTRDVSYFF----KESPPEAYNILFKGTR-KITLPYTGNYENLQTAAH
                                                                                                                                   LALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PS00275; SHIGA_RICIN; 1.
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                                                                                                                                                                                                                      VNFDLSTATAKTYTKFIEDFRATLPFSHKVYDIPLLYSTISDSRRFILLDLTSYAYETIS
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286 AA;
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32031 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23
286
                                                                                                                                                                                                                                                                                                                                                                         28.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   synthesis inhibitor; Hydrolase; Toxin; Signal;
                                                                                                                                                                                                                                                                                                                                             ; Score 272; DB 1;
; Pred. No. 5.7e-18;
39; Mismatches 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RIBOSOME-INACTIVATING PROTEIN MOMORDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3B89FF1AE6B25986 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      Length 286;
                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                                                                             Gaps
                                   181
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DP DP 141 KIRENIDLGLPALSSAITTLFYYNA-----QSAPSALLVLIQTTAEAARFKYIERHVAKY 195

182 IRYN 185

: | 196 VATN 199

Search completed: September 16, 2003, 11:46:04 Job time :  $7.59071~{\rm secs}$ 

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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Run on:
                                                                                                                                                                                                                                                                                            Database :
                                                               SPTREMBL_23:*
1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
5: sp_inverteb
6: sp_mammal:*
7: sp_mhc:*
8: sp_organel1
9: sp_phage:*
11: sp_virus:*
13: sp_virus:*
13: sp_vertebi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            830525 seqs, 258052604 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BLOSUM62
Gapop 10.0 , Gapext 0.5
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966
1 IFPKQYPIINFTTAGATVQS.....ARFQYIEGEMRTRIRYNRRS 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  September 16, 2003, 11:40:08; Search time 29.9877 Seconds (without alignments) 1617.791 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                     sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
                                                                                                                                  sp_organelle:*
sp_phage:*
                                                                                  sp_plant:*
sp_rodent:*
sp_virus:*
                                                                                                                                                                                       sp_invertebrate:*
sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                830525
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIE

Result No.	Score	Query Match I	Length DB	₽B	ID	Description
1	951	98.4	541	10	Q41174	Q41174 ricinus com
2	374.5	38.8	580	10	Q94BW3	Q94bw3 cinnamomum
ω	372.5	38.6	580	10	Q94BW4	Q94bw4 cinnamomum
4	370.5	38.4	581	10	Q94BW5	Q94bw5 cinnamomum
u	368.5	38.1	549	10	Q9FV22	Q9fv22 cinnamomum
0	334	34.6	289	10	Q94KE4	Q94ke4 trichosanth
7	332	34.4	289	10	Q41216	Q41216 trichosanth
æ	329.5	34.1	563	10	004367	004367 sambucus ni
9	326	33.7	247	10	Q9LRE3	Q9lre3 trichosanth
10	323.5	33.5	564	10	Q9AVR2	Q9avr2 sambucus eb
11	318.5	33.0	528	10	Q06076	-
12	317	32.8	270	10	Q8LPV7	Q8lpv7 trichosanth
13	310.5	32.1	252	10	Q38760	Q38760 abrus preca
14	307.5	31.8	563	10	Q945S2	Q945s2 sambucus ni
15	307.5	31.8	563	10	Q8GT32	Q8gt32 sambucus ni
16	305	31.6	270	10	Q41611	Q41611 trichosanth

444	41	39 40	38	36 7	35	ω 4-	ω W	ա ( N.F	<u>ب</u>	٠,	29	28	27	26	25	24	23	22	21	20	19	18	17
246.5 246.5 245.5	247 247	253 251	259	259	260	260	263	265	266.5	267	270	270	271	273	273	290.5	293.5	296.5	297.5	298.5	300.5	302	303.5
25.5	222	26	26	2 2	26	8	27	27	27	27.6	28.0	28.0	28.1	28.3	28.3	30.1	30.4	•	•	•	•	31.3	•
275	258 293	249	569	251 293	573	254	565	286	604	570	286	249	592	570	264	251	566	251	251	547	278	565	252
10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
Q8H1Y4 Q9M653	Q9S9E4 Q8VYU0	Q8RXH5 Q8RXH7	P93543	Q8LKQ4 08S452	Q8W2E8	Q8LKQ6	08W243	041257	09M654	022415	Q9FUV7	Q8LKQ5	Q8W2E7	Q41358	Q9FSH2	Q96235	004072	Q96237	Q96236	Q9M6E9	000980	004071	Q38761
000	200	0.00	q	<u>o</u> o	30	30	Q	2	0.0	o.	20	30	90	24	09	29	00	09	29	09	00	00	Q3
Q8h1y4 Q8h653	0959e4 08vyu0 08vy69	Q8rxh7	P93543	081kq4 08s452	Q8w2e8	31kq6	Q8w243	041257	Q9m654	022415	Q9fuv7	31kq5	Q8w2e7	Q41358	fsh2	Q96235	004072	Q96237	Q96236	Q9m6e9	0860	004071	Q38761
gynostemma polygonatum		viscum albu		jatropha cu			viscum albu	momordica c	polygonatum		momordica c	viscum albu	iris hollan	sambucus ni	momordic		sambu	abrus preca	abrus preca	abrus preca			abrus preca

# ALIGNMENTS

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
Yang Q., Gong Z.Z., Liu W.Y.;
"Molecular cloning of three type 2 RIP (ribosome-inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00458; RICIN; 2.
PROSITE; PS50231; RICIN_B_LECTIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00652; Ricin_B_lectin;
Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AY039803; AAK82460.1; -.
InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Type 2 ribosome-inactivating protein cinnamomin III precursor (EC 3.2.2.2) (rRNA N-glycosidase).
Cinnamomum camphora (Camphor tree).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheopl
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genes encoding cinnamomin proteins and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spermatophyta; Magnoliophyta; Laurales;
                                                                                                                                                                                                                                                                                       Local
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                                                  116 LEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PR00396; SHIGARICIN.
                                                                                                                                                                                                                                                                                       Similarity
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          LERVAGERREEILLGMDPLENAISALWISNL--NQQRALARSLIVVIQMVAEAVRFRFIE
                                                                                           ADSPYTLAYDYTNAYVVAYRTGSQSFFLREDNPD--PAIENLLPDTK-RYTFPFSGSYTD
                                                                                                                   AELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLETDVQNRYTFAFGGNYDR 115
                                                                                                                                                                            YQTVTFTTKNATKTSYTQFIEALRAQLASGEEPHGIPVMRERSTVPDSKRFILVELSNWA 92
                                                                                                                                                                                                                   YPIINFTTAGATVQSYTNFIRAVRGRLT------VLPNRVGLPINQRFILVELSN-H 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FQYIEGEMRTRIRYNRRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELSNHAELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFG
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal; Toxin.
                                                                                                                                                                                                                                                                                                                                                  580 AA;
                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                    64421 MW;
                                                                                                                                                                                                                                                                                   38.8%;
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94.9%;
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                                                                                                                                                                                                                                                                                   Score 374.5; DB 10; Length Pred. No. 3.7e-27;
                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.

TYPE 2 RIBOSOME-INACTIVATING PROTEIN
CINNAMOMIN III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 951; DB 10;
Pred. No. 2.7e-82;
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                                                                                                                                                                                                                                                                                                                                                  940D10F01E7FB558 CRC64;
                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ą
                                                                                                                                                                                                                                                               56;
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                                                                                                                                                      RESULT 4
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Q94BW4
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Type 2 ribosome-inactivating protein cinnamomin I p:
(EC 3.2.2.22) (TRNA N-glycosidase).
                                                                                                                                  Q94BW5
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EMBL; AY039802; AAK82459.1; -.
InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
Pfam; PF00652; Ricin_B_lectin; 6.
Pfam; PF00652; Ricin_B_lectin; 6.
Pfam; PF00161; RIP; 1.
PRINTS; PR00396; SHIGARICIN.
SMART; SM00458; RICIN_B_LECTIN; 2.
PROSITE; PS50231; RICIN_B_LECTIN; 2.
Hydrolase; Signal; TOXIN.
1 32 POTENTIAL.
                                                                                                               Q94BW5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cinnamomum camphora (Camphor tree).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; Laurales; Lauraceae; Ci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Type 2 ribosome-inactivating protein cinnamomin II precursor (EC 3.2.2.2) (FRNA N-glycosidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Molecular cloning of three type 2 RIP genes encoding cinnamomin proteins and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Yang Q., Gong Z.Z., Liu W.Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q94BW4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  patterns
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                                                                                                                                                                                                                                                                                                                          LERVAGELREEILLGMDPLENAISAL--WTSNLNQQRALARSLIVVIQMVAEAVRFRFIE
                                                                                                                                                                                                                                                                                                                                                               LEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIE 175
                                                                                                                                                                                                                                                                                                                                                                                                                                 AELSVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDR 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YPIINFTTAGATVQSYTNFIRAVRGRLTVLPNRVGLPI-----NQRFILVELSN-H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YQTVTFTTKNATKTSYTQFIEALRAQLASGEEPHGIPVMRDGSTVPDSKRFILVELSNWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             580 AA; 64265 MW;
                                                                                                                                  PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 372.5;
Pred. No. 5.7
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                                                                                                                                  PRT;
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                                                                                                                                  AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10;
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                          I precursor
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PRESULT Q9FV22 ID FV22 ID FV22 Q9 DT 011 DT 01 TYPE DE N. TYP
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Xie L., Liu W.-Y., Wang E.-D.;

"Molecular cloning of cinnamomin A-, B-chain and the expression, purification, characterization and mutagenesis of the A-Chain.";

Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.

-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND /

-!- SIMILARITY: BELONGS TO THE 28S RRNA.

-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMI
EMBL; AF259548; AAF68978.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O9FV22
O9FV22:
O9FV22:
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Type II ribosome-inactivating protein cinnamomin (E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cinnamomum camphora (Camphor tree). Eukaryota; Viridiplantae; Streptoph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00396; SHIGARICIN.
SMART; SM00458; RICIN; 2.
PROSITE; PS50231; RICIN_B_LECTIN;
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InterPro; IPR001574; RIP.
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Yang Q., Gong Z.Z., Liu W.Y.;
"Molecular cloning of three type 2 RIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae;
Spermatophyta; Magnolioph;
NCBI_TaxID=13429;
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fY: ENDOHYDROLYSIS OF THE
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yta; Laurales;
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Lauraceae; Cinnamomum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lauraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Embryophyta;
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                                                                            Matches
                                                                                     Query Match
Best Local :
                                                                                                                                                                               Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT (SPECIFIC ADBOSINE ON THE 28S RRNA.

-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY. EMBL; AF367252; AAK52960.1; -. InterPro; IPR001574; RIP.

Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                   Q94KE4;
                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
                                                                                                                                                                                                                                                                                                                                                  Trichosanthes kirilowii (Mongolian snake-gourd)
                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
Trichosanthin precursor
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Pfam; PF00161; RIP; 1
                                                                                                                                           Hydrolase; Signal; SIGNAL 1
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                                                                                                                       SEQUENCE
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                                                                                                                                  CHAIN
                                                                                                                                                                  PROSITE; PS00275; SHIGA_RICIN; 1.
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                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YRVRGSI 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIE
VSFRLSGATSSSYGVFISNLR---KALPNERKLYDIPLLRSSLPGSQRYALIHLTNYADE
                                                      INFTTAGATVQSYTNFIRAVRGRLTVLPN------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GEMRTRI 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LEGVAGERREEILLGMDPLENAISALWISNL--NQQRALARSLIVVIQMVAEAVRFRFIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AELSYTLALDYTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YQTVTFTTKKATKTSYTQFIEALRAQLASGEEPHGIPVMRERSTVPDSKRFILVELSNWA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               549 AA;
                                                                                                                      289 AA;
                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                        Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 60648 MW;
                                                                                                                         31706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38.1%;
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                                                                                       34.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B_lectin;
                                                                                                                                                                                                                                                                                                                                                                         19,
19,
23,
                                                                                                                      MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25;
                                                                            42;
                                                                    Pred. NO. 10
42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
3.2.2.22) (rRNA N-glycosidase)
                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 368.5;
Pred. No. 1.
                                                                                  Score 334; טש ב.
                                                                                                                                  POTENTIAL.
TRICHOSANTHIN
                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02607FE607CA44B0 CRC64;
                                                                                                                       A6D5602549CA5657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                289
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nes 57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10;
                                                                                                 10;
                                                                            49;
                                                      -RVGLPINQRFILVELSNHAEL
                                                                                                                         CRC64;
                                                                                                 Length 289;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            549;
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                                                                             22;
                                                                                                                                                                                                                                                                                                                              Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                  004367;
                  01-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Ribosome inactivating protein precursor (EC 3.2.2.22) (rRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 22, Last annotation update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Trichosanthin (EC 3.2.2.22) (TRNA N-9lycosidase).
TRICHOSANTHIN, TCS.
Trichosanthes kirilowii (Mongolian snake-gourd).
Trichosanthes kirilowii (Mongolian snake-gourd).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
N-glycosidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PR00396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zheng H., Wang B., Shaw P., Yeung H.;

"[Cloning and DNA sequencing of the gene encoding trichosanthin].";

I Chuan Hauch Pao 21:42-51(1994)

- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE
SPECIFIC ADENOSINE ON THE 285 RRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q41216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; S70176; AAB31048.1; -. HSSP; P09989; 1MRJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00161; RIP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94271613; PubMed=8003348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGE 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SVTLALDVTNAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLE 117
                                                                                                                                                                                                                                                                                                                                    IGKRV 198
                                                                                                                                                                                                                                                                                                                                                                                        MRTRI 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISVAIDVTSVYIMGYRAGDTSYFF---NEASATEAAKYVFKDAMRKVTLPYSGNYERLQ 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFTTAGATVQSYTNFIRAVRGRLTVLPN------RVGLPINQRFILVELSNHAEL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IGKRV 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSFRLSGATSSSYGVFISNLR---KALPNERKLYDIPLLRSSLPGSQRYALVHLTNYADE 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAAGKIRENIPLGLPALDSAITTLFYYNAN----SAASALMVLIQSTSEAARYKFIEQQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 289 AA; 31650 MW;
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                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 332; DB 10;
Pred. No. 1.6e-23;
                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    286AC14D48BCA175 CRC64;
                                                                                                                                                                                 563 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 289;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
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                                                                                                                                                                                                                                                                                                RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best
SEQUENCE FROM N.A.

Phan Van Chi, Nguyen Thuy Ha, Le Tran Binh;
Phan Van Chi, Nguyen Thuy Ha, Le Tran Binh;
"Genomic DNA Clone for mature typ-1 ribosome-inactivating protein from Trichosanthes sp. sample 01 Bac Kan 8-98 Vien CNSH (Hanoi).";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 25, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Trichobakin (EC 3.2.2.22) (IRNA N-glycosidase) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "The major elderberry (Sambucus nigra) fruit protein is a lectin derived from a truncated type 2 ribosome-inactivating protein."; plant J. 12:1251-1260(1997).

-i- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND AT ONE SPECIFIC ADENOSINE ON THE 28S RRNA.
                                                                                                            Spermatophyta; Magnoliophyta; eudicotyledons; eurosids I; Cucurbitales; Cucurbitaceae; Tricl
                                                                                                                                     Trichosanthes sp. Bac Kan 8-98.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00652; Ricin_B_lectin; Pfam; PF00161; RIP; 1. PRINTS; PR00396; SHIGARICIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sambucus nigra (European elder).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.
                                                                                             NCBI_TaxID=118182;
                                                                                                                                                                                                                                                                     Q9LRE3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50231; RICIN_B_LECTIN; PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00458; RICIN; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U76524; AAC15886.1; -. HSSP; P02879; 2AAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-98112023; PubMed-9450339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=4202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peumans W.J.
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                                                                                                                                                                                                                                                                                                                                                                                                       142
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                                                                                                                                                                                                                                                                                                                                                                                                                                    114 DRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQY 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88
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                                                                                                                                                                                                                                                                                                                                                                          IEGEMRTRIR 183
                                                                                                                                                                                                                                                                                                                                                                                                       DNLETAAGTRRESIELGPSPLDGAITSLYYDE-----SVARSLLVVIQMVSEAARFRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGNTYTLAVDYTNLYVVAFSANANSYFF-----KDATQLQKSNLFVGTR-QHTLPFTGNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YPSVSFNLAGAKSATYRDFLKNLRTIVATGTYEVNGLPVLRRESEVQVKNRFVLVLLTNY
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                                                                                                                                                                                                                                                                                                                                            IEQEVRRSLQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   298
563 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal; Toxin.
                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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563 R
62336 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred.
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RIBOSOME INACTIVATING PROTEIN, A CHAIN.
RIBOSOME INACTIVATING PROTEIN, B CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 329.5;
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                                                                                                               Trichosanthes
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                                                                                                                          core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                             Rosidae;
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Qy
Q9AVR2
ID Q9AVR
AC Q9AVR
AC Q9AVR
AC Q9AVR
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-S
CO Ribos
DE N-11S
CO Sambu
OC Eukar
OC Sperm
OC Aster
OC Aster
OC ASTER
RP SEQUE
RC TISSU
RA G1rbe
RC TISSU
RA G1rbe
RC -1- C
CC -1- S
CC -1- S
CC -1- S
CC TISSU
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DR HSSP;
DR HSSP;
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DR Inter
DR Ffam;
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DR PROSI
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Best Local S
Matches 72
                                          PROSITE; PS50231; RICIN_B_LECTIN; 2.
PROSITE; PS00275; SHIGA_RICIN; 1.
Glycosidase; Hydrolase; Signal; Toxin.
SIGNAL 1 25 POTENTIAL.
                                                                                                                                                                                                                                                                                                Girbes T., Iglesias R., Perez Y., Ferreras J.M., Citores L.;
"Molecular cloning of ebulin 1.";
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
-1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND SPECIFIC ANENOSINE ON THE 28S RRNA.
-1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMESE, P02879; 2AAI.
-1- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMESP; P02879; 2AAI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9AVR2;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-MAR-2003 (TrEMBLrel. 27,
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-i- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTEIN FAMILY.
EMBL; AB039324; BAA92530.1; -.
HSSP; P09989; 1MRJ.
                                                                                                                                                                                                      Pfam; PF00652; Ricin_B_lectin;
Pfam: PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; campanulids; Dipsacales; Adoxaceae; Sambucus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9AVR2
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PROSITE; PS00275; SHIGA_RICIN;
                                                                                                                                                                                                                                                   InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Leat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sambucus ebulus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-glycosidase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ribosome-inactivating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=28503;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
                                                                                                                                                 PF00161; RIP; 1.
S; PR00396; SHIGARIC; SM00458; RICIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKIRENIPLGLPALDSAITTLFYYNAN-----SAASALMVLIQSTSEAARYKFIEQQIGK 173
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247 AA;
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                                                                                                                                                                              SHIGARICIN.
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Last annotation update)
in precursor (EC 3.2.2.22) (rRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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EBULIN L A-CHAIN
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RESULT 11
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O06076
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OT 01-W
OC Euka
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OC eurc
OX NCBJ
RN (E1)
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Q06076;
Q1-NOV-1996
Q1-NOV-1996
Q1-MAR-2003
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01-NOV-1996 (TrEMBLrel. 23, Last sequence update)
01-NOV-1996 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Abrin-d (EC 3.2.2.2) (rRNA N-glycosidase) (Fragment).
Abrus precatorius (Indian licorice) (Crab's eye).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid.
Eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hung C.-H., Lee M.-C., Lee T.-C., Lin J.-Y.;
"Primary structure of three distinct isoabrins determined sequencing: conservation and significance.";
J. Mol. Biol. 229:263-267(1993).
-!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC SPECIFIC ADENOSINE ON THE 28S RRNA.
-!- SIMILARITY: BELONGS TO THE RIBOSOME-INACTIVATING PROTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; M98346; AAA32626.1;
HSSP; P11140; 1ABR.
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                                                                                                                                                                                                                                                                                                                                                   Hydrolase; Toxin.
                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50231; RICIN_B_LECTIN; PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00652; Ricin_B_lectin;
Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000772; Ricin_B_lectin.
InterPro; IPR001574; RIP.
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                                                                                                                                                                                                                                                                                                                                NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00458; RICIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00396; SHIGARICIN.
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                                                                                                                                                                                                                               Similarity
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RESIEVGIDVTNAYVVAYRAGSQSYFL---RDAPASASTYLFPGTQ-RYSLRFDGSYGDL
                            ELSYTLALDYTNAYVYGYRAGNSAYFFHPDNQEDAEAITHLFTDYQNRYTFAFGGNYDRL
                                                                                                                                NGDTVTSAVDVTNLYLVAFSANGNSYFF-----KDATELQKSNLFLGT-TQHTLSFTGNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YPSVSFNLAGAKSTTYRDFLKNLRDRVATGTYEVNGLPVLRRESEVQVKNRFVLVRLTNY
                                                                                                      QDQVIKFTTEGATSQSYKQFIEALRQRLTGGLIHDIPVLPDPTTVEERNRYITVELSNSE
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528 AA;
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58870 MW;
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Pred. No. 2.
                                                                                                                                                                                                                          Score 318.5;
Pred. No. 7.3
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                                                                                                                                                                                                                                                                                                         62ED42FB8FFE60F8 CRC64;
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RESULT 12
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Matches
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               01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Abrin-E (RRNA N-glycosidase) (EC 3.2.2.22) (Fragment).
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01-OCT-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
Trichosanthin precursor
                                                                                                              Q38760;
                                                                                                                                Q38760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trichosanthes kirilowii (Mongolian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8LPV7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00396; SHIGARICIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00161; RIP; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=3677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nterPro; IPR001574; RIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                     181
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                                                                                                                                                                                                                                                                                                                                                                      121 GNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 LALDVINAYVVGYRAGNSAYFFHPDNQEDA-EAITHLFTDVQNRYTFAFGGNYDRLEQLA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25
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                                                                                                                                                                                                                                            RV -
                                                                                                                                                                                                                                                                                   RI
                                                                                                                                                                                                                                                                                                                                GKIRENIPLGLPALDSAITTLFYYNAN-----SAASALLVLIQSTAEAARYKFIEQQIGK 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFTTAGATYQSYTNFIRAVRGRLTYLPNRVGLPI-----NQRFILVELSNHAELSVT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RVGVSIR 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VSFRLSGATSSSYGVFISNLRKALPYEKKLYDIPLLRSSLSGSQRYALIYLTNYADETIS 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMRTRIR 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              270
270 AA;
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                                                                                                                                                                                                                                                                                     182
                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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22,
23,
EC
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Last annotation update)
3.2.2.22) (rRNA N-glycosidase)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 317; DB 1
Pred. No. 4e-22;
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                                                                                                                                  PRT;
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                                                                                                                                252 AA
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RESULT 14
Q945S2
ID Q945S
AC Q945S
AC Q945S
DT 01-DE
DT 01-MA
DT 01-MA
DE Ribos
DE N-91y
GN AVI.
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                                                                                                                   094552;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; Prouse, ...,
PRINTS; PRO0396; SHIGARICIN.
PROSITE; PS00275; SHIGA_RICIN; 1.
PROSITE; PS00275; SHIGA_RICIN; 1.
Hydrolase; Glycosidase; Toxin; Repeat; Glycoprotein; Lectin.
Hydrolase; Glycosidase; Toxin; Repeat; Glycoprotein; Lectin.
Hydrolase; Glycosidase; Toxin; Repeat; Glycoprotein; Lectin.
Hydrolase; Glycosidase; Toxin; A CHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chains.";

J. Biol. Chem. 266:6848-6852(1991).

-!- FUNCTION: THE A CHAIN IS RESPONSIBLE FOR INHIBITING PROTEIN SYNTHESIS THROUGH THE CATALYTIC INACTIVATION OF 60S RIBOSOMAL SUBUNITS BY REMOVING ADENINE FROM POSITION 4,324 OF 28 S RNA ABRIN-A IS MORE TOXIC THAN RICIN.

-!- FUNCTION: THE B CHAIN IS A GALACTOSE-SPECIFIC LECTIN THAT FACILITATES THE BINDING OF ABRIN TO THE CELL MEMBRANE THAT PRECEDES ENDOCYTOSIS.
Sambucus nigra (Buropean elder).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
Asteridae; campanulids; Dipsacales; Adoxaceae; Sambuc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Abrus precatorius (Indian licorice) (Crab's eye).
Eukaryota; Viridiplantae; Streptophyta; Entryophyta; Tracheop
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
eurosids I; Fabales; Fabaceae; Papilionoideae; Abreae; Abrus.
                                                                                                          N-glycosidase).
                                                                                                                                                                                                                                            Q945S2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001574; RIP. Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X54872; CAA38654.1; HSSP; P11140; LABR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONSISTS OF 3 HOMOLOGOUS SUBDOMAINS (ALPHA, BETA, GAMMA).
-!- SIMILARITY: TO OTHER BACTERIAL AND PLANTS RIBOSOME-INACTIVATING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIFIC ADENOSINE ON THE 28S RRNA.

-!- SUBUNIT: DISULFIDE-LINKED DIMER OF A AND B CHAI-
-!- DOMAIN: THE B CHAIN IS COMPOSED OF TWO DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Evensen G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=91201329; PubMed=2016300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-LEAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=3816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Poirect molecular cloning and expression of two distinct abrin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF THE N-GLYCOSIDIC BOND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEINS. BELONGS TO TYPE
                                                                                                                                                                                                                                                                                                                                                                                             181 RIR 183
                                                                                                                                                                                                                                                                                                                                                                                                                                        122 HQTREQISLGLQALTHAIS---FLRSGASNDEEKARTLIVIIQMASEAARYRYISNRVGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 GNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQYIEGEMRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 TLALDVTNAYVVGYRAGNSAYFFHPDNQEDAEAITHLFTDVQNRYTFAFGGNYDRLEQLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVGIDVTNAYVVAYRAGSQSYFL---RDAPASASTYLFTGTQ-RYSLRFDGSYGDLERWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IKFSTEGATSQSYKQFIEALRERLRGGLIHDIPVLRDPTTVEERNRYITVELSNSERESI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFTTAGATVQSYTNFIRAVRGRL-----TVLPNRVGLPINQRFILVELSNHAELSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     252
252 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   252
28309 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.1%;
43.2%;
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                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BBFC846B9E92B5DE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67;
                        core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                             Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosidae;
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121

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RESULT QRET32 ID QRET32 ID QRET32 QRE
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Best Local
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     Matches
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Ol-MAR-2003 (TrEMBLrel. 23, Created)
Ol-MAR-2003 (TrEMBLrel. 23, Last sequence update)
Ol-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Type 2 ribosome-inactivating protein nigrin l precursor
(EC 3.2.2.22)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Girbes T., Arias F.J., Antolin P.;

"Characterization and molecular cloning of Nigrin 1, a type two ribosome-inactivating protein from leaves of elder (Sambucus nig Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AF249280; AAN86130.1; -.

Hydrolase; Glycosidase.
                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Streptidae; campanulids; Dipsacales; Adoxaceae; Sambucus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS50231; RICIN_B_LECTIN; PROSITE; PS00275; SHIGA_RICIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00396; SHIGARICIN. SMART; SM00458; RICIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00652; Ricin_B_lectin; 6.
Pfam; PF00161; RIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                     Sambucus nigra (European elder).
Eukaryota; Viridiplantae; Strept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q8GT32
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                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                         TISSUE=Leaf;
                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hydrolase;
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                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IEQEVRRSLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IEGEMRTRIR 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNLETAANTRRESIELGPSPLDGAITSLYHGD-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NGNTVTLAVDVTNLYVVAFSGNANSYFF-----KDATEVQKSNLFVGTKQN-TLSFTGNY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YPSVSFNLDGAKSATYRDFLSNLRKTVATGTYEVNGLPVLRRESEVQVKSRFVLVPLTNY
                                                                                                  Glycosidase.
563 AA; 62173 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Toxin. 563 AA; 62242 MW; 07F7CBEDCF33BF10 CRC64;
     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                       31.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.8%; Score 307.5; DB 1 38.4%; Pred. No. 8.9e-21;
36;
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                         Score 307.5; DB : Pred. No. 8.9e-21
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                                                                                                    OEB236421FC5E04F CRC64;
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     Mismatches
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                                                 DB 10;
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     56;
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     Indels
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                                              Length 563;
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     25;
                                                                                                                                                                                                 nigra).";
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                                                                                                                   DNLETAANTRRESIELGPSPLDGAITSLYHGD-----SVARSLLVVIQMVSEAARFRY
                                                                                                                                                                       YPIINETTAGATVQSYTNFIRAVR------GRLTVLPNRVGLPINQRFILVELSNH
IEQEVRRSLQ
                        IEGEMRTRIR 183
                                                                             DRLEQLAGNLRENIELGNGPLEEAISALYYYSTGGTQLPTLARSFIICIQMISEAARFQY
                                                                                                        NGNTVTLAVDVTNLYVVAFSGNANSYFF-----KDATEVQKSNLFVGTKQN-TLSFTGNY
                                                                                                                                                           YPSVSFNLDGAKSATYRDFLSNLRKTVATGTYEVNGLPVLRRESEVQVKSRFVLVPLTNY
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Search completed: September 16, 2003, 11:49:15 Job time: 30.9877 secs

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